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OM protein - protein search, using sw model

Run on: June 24, 2003, 21:27:56 ; Search time 7.74147 Seconds
(without alignments)
1007.182 Million cell updates/sec

Title: US-09-813-453A-4
Perfect score: 1343
Sequence: 1 MLLTIDVGNTHVTVLGLFDGE.....EPWLTLMGLRLVYERNVSRM 265

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA: *
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep: *
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep: *
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep: *
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep: *
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep: *
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	93	6.9	4928	4 US-09-036-987A-5	Sequence 5, Appli
2	93	6.9	4928	4 US-09-370-700-5	Sequence 5, Appli
3	91.5	6.8	1113	4 US-09-629-616-3	Sequence 3, Appli
4	91	6.8	521	4 US-09-134-001C-5639	Sequence 5639, Ap
5	89	6.6	361	3 US-09-028-934-30	Sequence 30, Appl
6	88.5	6.6	3724	2 US-08-804-227C-10	Sequence 10, Appl
7	88.5	6.6	3724	2 US-08-804-198-4	Sequence 4, Appli
8	87	6.5	234	4 US-09-134-001C-3362	Sequence 3362, Ap
9	86.5	6.4	361	2 US-08-729-214-25	Sequence 25, Appl
10	86.5	6.4	361	3 US-09-028-934-25	Sequence 25, Appl
11	85	6.3	731	2 US-08-911-364-1	Sequence 1, Appli
12	85	6.3	733	4 US-08-464-700-2	Sequence 2, Appli
13	85	6.3	3567	2 US-07-642-734C-4	Sequence 4, Appli
14	85	6.3	3567	3 US-08-439-009A-4	Sequence 4, Appli
15	84	6.3	549	3 US-08-886-886-13	Sequence 13, Appl
16	83.5	6.2	3519	4 US-09-428-517-4	Sequence 4, Appli
17	83.5	6.2	4150	4 US-09-428-517-2	Sequence 2, Appli
18	83	6.2	201	2 US-08-911-364-2	Sequence 2, Appli
19	83	6.2	330	4 US-09-134-001C-3582	Sequence 3582, Ap
20	81.5	6.1	432	2 US-08-677-049-8	Sequence 8, Appli
21	81.5	6.1	792	2 US-08-678-039A-40	Sequence 40, Appl
22	80.5	6.0	819	4 US-09-651-656-15	Sequence 15, Appl
23	80.5	6.0	819	4 US-09-650-855-15	Sequence 15, Appl
24	80	6.0	355	4 US-08-818-112-79	Sequence 79, Appl
25	80	6.0	355	4 US-08-818-111-80	Sequence 80, Appl
26	80	6.0	355	4 US-09-056-556-79	Sequence 79, Appl
27	80	6.0	355	4 US-09-072-596-80	Sequence 80, Appl

28	80	6.0	769	3 US-09-320-878-12	Sequence 12, Appl
29	80	6.0	809	4 US-09-105-537-24	Sequence 24, Appl
30	80	6.0	866	3 US-09-040-843-2	Sequence 2, Appli
31	80	6.0	866	4 US-09-621-855-2	Sequence 2, Appli
32	80	6.0	3782	4 US-09-105-537-4	Sequence 4, Appli
33	80	6.0	4545	2 US-08-804-227C-14	Sequence 14, Appl
34	80	6.0	4550	2 US-08-804-227C-8	Sequence 8, Appli
35	80	6.0	4550	2 US-08-804-198-2	Sequence 2, Appli
36	80	6.0	15281	2 US-08-471-119A-2	Sequence 2, Appli
37	79.5	5.9	263	4 US-09-134-001C-4512	Sequence 4512, Ap
38	79.5	5.9	493	4 US-09-177-349-5	Sequence 5, Appli
39	79.5	5.9	635	4 US-08-931-608A-5	Sequence 5, Appli
40	79.5	5.9	1529	2 US-08-728-470-10	Sequence 10, Appl
41	79.5	5.9	1529	4 US-08-719-641-10	Sequence 10, Appl
42	79.5	5.9	1600	2 US-08-617-697-10	Sequence 10, Appl
43	79	5.9	3739	3 US-09-320-878-2	Sequence 2, Appli
44	79	5.9	3739	4 US-09-105-537-33	Sequence 33, Appl
45	79	5.9	11877	4 US-09-105-537-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-036-987A-5
; Sequence 5, Application US/09036987A
; Patent No. 6143526
; GENERAL INFORMATION:
; APPLICANT: Baltz, Richard H.
; APPLICANT: Broughton, Mary C.
; APPLICANT: Crawford, Kathryn P.
; APPLICANT: Madduri, Krishnamurthy
; APPLICANT: Merlo, Donald J.
; APPLICANT: Treadway, Patti J.
; APPLICANT: Turner, Jan R.
; APPLICANT: Waldron, Clive
; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
; TITLE OF INVENTION: Production
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dow Agrosciences LLC Patent Department
; STREET: 9330 Zionsville Road
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/036,987A
; FILING DATE: 09-MAR-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stuart, Donald R
; REGISTRATION NUMBER: 28,479
; REFERENCE/DOCKET NUMBER: 50,608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317)337-4816
; TELEFAX: (317)337-4847
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4928 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-036-987A-5

Query Match 6.9%; Score 93; DB 4; Length 4928;
Best Local Similarity 24.7%; Pred. No. 3.1;
Matches 54; Conservative 30; Mismatches 77; Indels 58; Gaps 11;

QY 13 VLGLFDGEDIVEHW-RIS-----TDSRRTADELAVLLQGLMGHPLLGD 56
: | | | : | | | : | | : | | : | | :
Db 2493 IAGRLDGGGIRSRWLRVSHAFSHRMDPMLAEFTIARSVDYRS---SGLPIVSTLTGE- 2548
: | | : | | : | | : | | : | | : | | :
QY 57 LGDGIDGIAICATVPSVLHELREVTTRYGDPVAVLVEPGVKTGVPILTDPHPKEVGADRI 116
: | | : | | : | | : | | : | | : | | :
Db 2549 ----LDEVGMPATPEYWVRQVREPVR--FADGVAALAAHGVSTVV-----EVGPDGV 2594
: | | : | | : | | : | | : | | : | | :
QY 117 INAV----AAVELYGGPAIVV-----DFGTATTFDA-VSARG-----EYIGGVIAPI 157
: | | : | | : | | : | | : | | : | | :
Db 2595 LSALVQECAGSDQGGRVAAVPLMRNDRDEAHTVTTALAQIHVRGAEDVDRSFFAGTGAK 2654
: | | : | | : | | : | | : | | : | | :
QY 158 GIEISVEALGVKGAQLRKIEVARPRSVIGKNTVEAMQSG 196
: | | : | | : | | : | | : | | : | | :
Db 2655 QVELPTYAF-----QRQRYWLDSPSEPVGQSADPARQSG 2688
: | | : | | : | | : | | : | | : | | :

RESULT 2
US-09-370-700-5
Sequence 5, Application US/09370700
Patent No. 6274350
GENERAL INFORMATION:
APPLICANT: Baltz, Richard H
APPLICANT: Broughton, Mary C
APPLICANT: Crawford, Kathryn P
APPLICANT: Madduri, Krishnamurthy
APPLICANT: Treadway, Patti J
APPLICANT: Turner, Jan R
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
FILE REFERENCE: 50489 DIV1
CURRENT APPLICATION NUMBER: US/09/370,700
CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: US 09/36987
EARLIER FILING DATE: 1998-03-09
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 4928
TYPE: PRT
ORGANISM: Saccharopolyspora spinosa
US-09-370-700-5

Query Match 6.9%; Score 93; DB 4; Length 4928;
Best Local Similarity 24.7%; Pred. No. 3.1;
Matches 54; Conservative 30; Mismatches 77; Indels 58; Gaps 11;
13 VLGLFDGEDIVEHW-RIS-----TDSRRTADELAVLLQGLMGHPLLGD 56
: | | | : | | | : | | : | | : | | :
2493 IAGRLDGGGIRSRWLRVSHAFSHRMDPMLAEFTIARSVDYRS---SGLPIVSTLTGE- 2548
: | | : | | : | | : | | : | | : | | :
QY 57 LGDGIDGIAICATVPSVLHELREVTTRYGDPVAVLVEPGVKTGVPILTDPHPKEVGADRI 116
: | | : | | : | | : | | : | | : | | :
Db 2549 ----LDEVGMPATPEYWVRQVREPVR--FADGVAALAAHGVSTVV-----EVGPDGV 2594
: | | : | | : | | : | | : | | : | | :
QY 117 INAV----AAVELYGGPAIVV-----DFGTATTFDA-VSARG-----EYIGGVIAPI 157
: | | : | | : | | : | | : | | : | | :
Db 2595 LSALVQECAGSDQGGRVAAVPLMRNDRDEAHTVTTALAQIHVRGAEDVDRSFFAGTGAK 2654
: | | : | | : | | : | | : | | : | | :
QY 158 GIEISVEALGVKGAQLRKIEVARPRSVIGKNTVEAMQSG 196
: | | : | | : | | : | | : | | : | | :
Db 2655 QVELPTYAF-----QRQRYWLDSPSEPVGQSADPARQSG 2688
: | | : | | : | | : | | : | | : | | :

RESULT 3
US-09-629-616-3
Sequence 3, Application US/09629616
Patent No. 6255086
GENERAL INFORMATION:
APPLICANT: KAWABARA, Yoko
APPLICANT: HASHIGUCHI, Kenichi
APPLICANT: NAKAMATSU, Tsuyoshi

APPLICANT: KURAHASHI, Osamu
APPLICANT: MORI, Yukiko
APPLICANT: ITO, Hisao
TITLE OF INVENTION: CARBAMOYL-PHOSPHATE SYNTHETASE GENE OF CORYNEFORM
FILE REFERENCE: OP945CIP
CURRENT APPLICATION NUMBER: US/09/629,616
CURRENT FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 1113
TYPE: PRT
ORGANISM: Brevibacterium lactofermentum
US-09-629-616-3
Query Match 6.8%; Score 91.5; DB 4; Length 1113;
Best Local Similarity 24.0%; Pred. No. 0.49;
Matches 61; Conservative 25; Mismatches 79; Indels 89; Gaps 13;
QY 28 ISTDSRRTADELAVLLQGLMGHPLLGDGLGIDGIAICATVPSVLHELREVTTRYGD 87
: | | | : | | | : | | : | | : | | :
Db 618 VSTD-YDTADRLY-----FEPLTFEDVMEVYHAEQAQSGTVAGVIVQLG-----GQ 661
: | | : | | : | | : | | : | | : | | :
QY 88 VPAYLVEPGVKTGVPILTDPK--EUGADR-IINAAVELYGGPAIVVDFGTATTFDAV 144
: | | : | | : | | : | | : | | : | | :
Db 662 TPLGLADRLKKAGVPVIGTSPEAIDMAEDRGEFALLNREQLPAPA-----FGTATSFEEA 717
: | | : | | : | | : | | : | | : | | :
QY 145 SARGEYIGGVIAPIAGIEISVEALGVKGAQLRKIEVARPRSVIGKNTVEAMQSGVIVGFAGQ 204
: | | : | | : | | : | | : | | : | | :
Db 718 RTVAD-----EISYPVL-----VRPSYVLGGRGME-----IVYDEA-S 749
: | | : | | : | | : | | : | | : | | :
QY 205 VDGVVNRMARLADDPD-----DVTVIATG----- 229
: | | : | | : | | : | | : | | : | | :
Db 750 LEDYINR-ATELSSDHPVLVDRFLDNAIEIDVDALCDGDEVYLAGVMEHIEEAGIHS GDS 808
: | | : | | : | | : | | : | | : | | :
QY 230 --GLAPMVLGESSV 241
: | | : | | : | | : | | : | | : | | :
Db 809 ACALPPMTLGAQDI 822
: | | : | | : | | : | | : | | : | | :

RESULT 4
US-09-134-001C-5639
Sequence 5639, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5639
LENGTH: 521
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5639

Query Match 6.8%; Score 91; DB 4; Length 521;
Best Local Similarity 22.6%; Pred. No. 0.18;
Matches 68; Conservative 51; Mismatches 88; Indels 94; Gaps 17;
QY 22 IVEHWRIIS-----TDSRRTADELAVLLQGLMGHPLLGD 54
: | | : | | : | | : | | : | | : | | :
Db 36 IIEHIQLSFIALFIATLIAVPIAILLTKTKLSEIVMNIAAVLQTIPTSLALLGLMIPFG 95
: | | : | | : | | : | | : | | : | | :
QY 55 DELGDGIDGIAICATVPSVLHELREVTTRYGDPVAVLVEPGVKTGVPILTDPHPKEVGAD 114
: | | : | | : | | : | | : | | : | | :

Db 96 --IG-----RLPAIALVYALLPILRNTY-----TGIKEVDPSLIBAAKGIGM- 137

QY 115 RIINAAVAEL-----YGG--PAIVVDFGTATTFDAVSARGEYIGGVIAPIGIEISVEA 165

Db 138 KPLRLTKVELPIAMPVIMAGIRTAMVLIIGTATLAALIGAGG--LGDLLILGIDRNSA 195

QY 166 LGVKG-----QLRKIE-VARPRSVIGKNTV-----EAMQSGIVYGF 201

Db 196 LILIGAIPAALLAIFDFILRYMERLSYKKLLISLGTIVIVIIAIAIPMAAQGDKITF 255

QY 202 AGQV---DGVVNRMARELADDDPDDVTVIATGGLAPMVLGESSVI-----DEHEPWLTLM 252

Db 256 AGKLGSEPSIITNMVKILIEEDTDDTVEVKDG-----MGKTSFLFNALKSDEIDGYLEFT 310

QY 253 G 253

Db 311 G 311

RESULT 5

S-09-028-934-30

; Sequence 30, Application US/09028934

; Patent No. 6117670

; GENERAL INFORMATION:

; APPLICANT: Ligon, James M.

; APPLICANT: Hill, Dwight S.

; APPLICANT: Lam, Steven T.

; APPLICANT: Hammer, Philip E.

; APPLICANT: van Pee, Karl-Heinz

; APPLICANT: Kirner, Sabine

; APPLICANT: Young, Thomas R.

; TITLE OF INVENTION: Pyrrolnitrin Biosynthesis Genes and Uses

; TITLE OF INVENTION: Thereof

; NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: No. 6117670artis Corporation

; STREET: 3054 Cornwallis Road

; CITY: Research Triangle Park

; STATE: NC

; COUNTRY: USA

; ZIP: 27709

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/028,934

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/729,214

; FILING DATE: 09-OCT-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/258,261

; FILING DATE: 08-JUN-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Meigs, J. Timothy

; REGISTRATION NUMBER: 38,241

; REFERENCE/DOCKET NUMBER: CGC1506/CIP7

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 919-541-8587

; TELEFAX: 919-541-8689

; INFORMATION FOR SEQ ID NO: 30:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 361 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-028-934-30

Query Match 6.6%; Score 89; DB 3; Length 361;

Best Local Similarity 22.6%; Pred. No. 0.17;

Matches 60; Conservative 35; Mismatches 93; Indels 78; Gaps 13;

QY 4 TIDVGNTHTVLGLFDGEDIVVHWRISTDSRRRTADELAVLLQGLMGHPLLGLDELGDIDG 63

Db 124 TADAQRSYT--GLGDEAHLLSVRISMASLEAAIALTVELYDV---PLRSPAFEEGCV 177

QY 64 IA--ICATVPSVLHRELVTRRYGVDVPAVLVEPGVKTG-----VPIL----- 104

Db 178 LA AHLQKMVESIVYAYRFPQVFFYDELRFYEP-IRVGGRSYLGPGAVEMPLFVLEHVL 236

QY 105 ----TDHP-----KEVGADRIINAAV-ELYGGPAIVVD--FGTATTFDAVSARGEYIG 152

Db 237 WGSQSDHPAYLEFKETYPVLPAPRAIYARFAGQALVDVRLGEA---QAARERGEVPG 293

QY 153 GVIAPGIEISVEALGVKQALRKIEVARPRSVIGKNTVEAMQSGIVYGFAGQVDGVVNRM 212

Db 294 AGLA-ALERIFEIL-----LHFRAPHLKLAERTYAAGQTG----- 327

QY 213 ARELADDDDDVTVIATGGLAPMVLGE 238

Db 328 -----PTIGSGGYAPSMGLD 342

RESULT 6

US-08-804-227C-10

; Sequence 10, Application US/08804227C

; Patent No. 5876991

; GENERAL INFORMATION:

; APPLICANT: DeHoff, Bradley S.

; APPLICANT: Kuhstoss, Stuart A.

; APPLICANT: Rosteck, Paul R., Jr.

; APPLICANT: Sutton, Kimberly L.

; TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: THOMAS G. PLANT 1501

; STREET: LILLY CORPORATE CENTER

; CITY: INDIANAPOLIS

; STATE: IN

; COUNTRY: USA

; ZIP: 46285

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: ASCII(DOS) Text only

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/804,227C

; FILING DATE: February 21, 1997

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Plant, Thomas, G.

; REGISTRATION NUMBER: 35,784

; REFERENCE/DOCKET NUMBER: X-8231

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 317-276-2459

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3724 amino acids

; TYPE: amino acid

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

US-08-804-227C-10

Query Match 6.6%; Score 88.5; DB 2; Length 3724;

Best Local Similarity 24.1%; Pred. No. 6.3;

Matches 77; Conservative 38; Mismatches 99; Indels 105; Gaps 19;

QY 2 LLTIDVGNTHTVLGLFDGEDIVVHWRISTDSRRRTA-DELAVALLQ----- 44

Db 983 LLIVPTGDQYTALA-----DTLEQAVASFGGTVRRVAFDPARTGRAELFGLLETEINGDT 1037

QY 45 -----GLMGM-----HPLLGLDELGDIDGICATVPSV--LHELREVTTRYGDVP 89

Db 1038 AVTGVVSLGLCTDGRPDHPAV-----PVAVTATLALVQALADLGSTAPLWTVTCG 1088
QY 90 AVLVEPGVKTGPILTDPKKEVGADRI-INAVAAVEL---YGGPAIVVDFGT---ATTFD 142
Db 1089 AVATAP-----DELPCCTAGAQWLGLGRVAAALELPEVWGG---LIDLPARPDARVLD 1136
QY 143 AVSARGEYIGGVIA-PGIE--ISVEALGVKGAQ-LRKIEVARPRSVIGKNTVEAMQSGIV 198
Db 1137 R-----LAGVLAEPGGEDQIAVRMAGVFGRRVLRNPADSRPPAWRARGTVL----- 1182
QY 199 YGFAGQVDGVVNRMARLADD-----PDDVTVIATGGLAPMVL-----GE 238
Db 1183 --IAGDLTTPVGRVLSLLEDGADRVVLAGPDAPAAAGLTVGSLVPVRCDTVTDRAAL 1240
QY 239 SSVIDEHPEWLTLMGLRLV 257
Db 1241 AALLDEHAPTVAHVAPPLV 1259

RESULT 7
US-08-804-198-4
; Sequence 4, Application US/08804198
; Patent No. 5945320
; GENERAL INFORMATION:
; APPLICANT: Burgett, Stanley G.
; APPLICANT: Kuhstoss, Stuart A.
; APPLICANT: Rao, Nagaraja R.
; APPLICANT: Richardson, Mark A.
; APPLICANT: Rostock, Paul R., Jr.
; TITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PAUL R. CANTRELL 1138
; STREET: LILLY CORPORATE CENTER
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,198
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CANTRELL, PAUL R.
; REGISTRATION NUMBER: 36,470
; REFERENCE/DOCKET NUMBER: P9113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-3885
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3724 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-804-198-4

Query Match 6.6%; Score 88.5; DB 2; Length 3724;
Best Local Similarity 24.1%; Pred. No. 6.3;
Matches 77; Conservative 38; Mismatches 99; Indels 105; Gaps 19;
QY 2 LLTIDVGNTHTVLGLFDGEDIVEH-----WRISTDSRRTA-DELAVALLO----- 44
Db 983 LLIVPTGDQYTALA-----DTLEQAVASFGGTVRRVAFDPARTGRAELFGLLETEINGDT 1037
QY 45 -----GLMGM-----HPLLGDGLGDGIDGIAICATVPSV--LHELREVTTRYGDDVP 89
Db 1038 AVTGVVSLGLCTDGRPDHPAV-----PVAVTATLALVQALADLGSTAPLWTVTCG 1088

QY 90 AVLVEPGVKTGPILTDPKKEVGADRI-INAVAAVEL---YGGPAIVVDFGT---ATTFD 142
Db 1089 AVATAP-----DELPCCTAGAQWLGLGRVAAALELPEVWGG---LIDLPARPDARVLD 1136
QY 143 AVSARGEYIGGVIA-PGIE--ISVEALGVKGAQ-LRKIEVARPRSVIGKNTVEAMQSGIV 198
Db 1137 R-----LAGVLAEPGGEDQIAVRMAGVFGRRVLRNPADSRPPAWRARGTVL----- 1182
QY 199 YGFAGQVDGVVNRMARLADD-----PDDVTVIATGGLAPMVL-----GE 238
Db 1183 --IAGDLTTPVGRVLSLLEDGADRVVLAGPDAPAAAGLTVGSLVPVRCDTVTDRAAL 1240
QY 239 SSVIDEHPEWLTLMGLRLV 257
Db 1241 AALLDEHAPTVAHVAPPLV 1259

RESULT 8
US-09-134-001C-3362
; Sequence 3362, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3362
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3362

Query Match 6.5%; Score 87; DB 4; Length 234;
Best Local Similarity 24.7%; Pred. No. 0.15;
Matches 48; Conservative 27; Mismatches 69; Indels 50; Gaps 9;
QY 54 GDELGDGIDGIAICATVPSVLHELREVTTRYGVDVPAVLVEPGVKTGPILTDPKKEVGA 113
Db 66 GDIINFFLEPATICFAIP--LYRKREVLKKYV-----LQIFGGIAVGTII-----A 109
QY 114 DRIINAVAAVELYGGPAIVVDFGTATTFDAVSARGEYIGG-----VIAPGIEISVEA 165
Db 110 LLLIYLVAITFFQGNQIIASMLPOAATTAIALPVSDGIGGVKELTSILAVILNAVVIS--A 167
QY 166 LGVKGAQLRKIE--VARPRSVIGKNTVEAMQSGIVYGFAGQVDGVVNRMARLADDDV 223
Db 168 LGAKIVKLFKISNPFIAR-----GLALGTSHTLGV--AAKELGETEESM 210
QY 224 TVIATGGLAPMVLG 237
Db 211 -----GSIIVVIG 219

RESULT 9
US-08-729-214-25
; Sequence 25, Application US/08729214
; Patent No. 5817502
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M.
; APPLICANT: Hill, Dwight Steven
; APPLICANT: Ryals, John Andrew
; APPLICANT: Hammer, Phillip E.
; APPLICANT: van Pee, Karl-Heinz
; APPLICANT: Kirner, Sabine
; TITLE OF INVENTION: Genes for the synthesis of

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/642,734C
FILING DATE: 17-JAN-91
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Danckers, Andreas M
REGISTRATION NUMBER: 32652
REFERENCE/DOCKET NUMBER: 4952.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-9396
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3567 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
-S-07-642-734C-4

Query Match 6.3%; Score 85; DB 2; Length 3567;
Best Local Similarity 26.6%; Pred. No. 14;
Matches 69; Conservative 30; Mismatches 102; Indels 58; Gaps 16;
QY 20 EDIVEHWRISTDSRRRTADELAVLLQGLMGHPLLGLDELGDGI--DGIAICATVPSV---- 73
Db 3190 EDLGASAEIAACDTADRDALSALLDGL--PRPLTGVVHAAGVLADGLVTSIDEPAVEQVL 3247
QY 74 -----LHELREVTRR-----YYGDVPAVLVEPGVKGTGVPILTDHPKVEGADRIINAV 120
Db 3248 RAKVDAAWNHLHETANTGLSFFVLFSSAASVLAGPG--QGV-----YAAANESLNA 3297
QY 121 AAVELYGG-PAIVVDFGT-ATTFDAVSARGEYIG--GVIAPGIEISVEALGVKGAQLRK- 175
Db 3298 AALRRTRGLPAKALGWGLWAQASEMTSGLGDRIARTGVAALPTE---RALALFDSALRRG 3354
QY 176 IEVARP-----RSVIGK-NTVEAMQSGIVYG---FAGQVD---GVVNRMARLADDDPDDV 223
Db 3355 GEVVFPLSINRSALRRAEFVPEVLRGMVRAKLRAAGQAEAAAGPNVVDRLAGRSESD---- 3410
QY 224 TVIATGGLAPMVLGESSVI 242
Db 3411 ---QVAGLAELVRSAAA 3426

RESULT 14
US-08-439-009A-4
Sequence 4, Application US/08439009A
Patent No. 6004787
GENERAL INFORMATION:
APPLICANT: Donadio, S
APPLICANT: Katz, L
APPLICANT: Mcalpine, J B
TITLE OF INVENTION: Method of Directing Biosynthesis of
TITLE OF INVENTION: Specific Polyketides
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven F. Weinstock
STREET: Abbott Laboratories D377/AP6D-2 One Abbott
STREET: Park Rd
CITY: Abbott Park
STATE: IL
COUNTRY: US
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/439,009A
FILING DATE: 11-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Casuto, Dianne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 4952.US.D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3567 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-439-009A-4

Query Match 6.3%; Score 85; DB 3; Length 3567;
Best Local Similarity 26.6%; Pred. No. 14;
Matches 69; Conservative 30; Mismatches 102; Indels 58; Gaps 16;
QY 20 EDIVEHWRISTDSRRRTADELAVLLQGLMGHPLLGLDELGDGI--DGIAICATVPSV---- 73
Db 3190 EDLGASAEIAACDTADRDALSALLDGL--PRPLTGVVHAAGVLADGLVTSIDEPAVEQVL 3247
QY 74 -----LHELREVTRR-----YYGDVPAVLVEPGVKGTGVPILTDHPKVEGADRIINAV 120
Db 3248 RAKVDAAWNHLHETANTGLSFFVLFSSAASVLAGPG--QGV-----YAAANESLNA 3297
QY 121 AAVELYGG-PAIVVDFGT-ATTFDAVSARGEYIG--GVIAPGIEISVEALGVKGAQLRK- 175
Db 3298 AALRRTRGLPAKALGWGLWAQASEMTSGLGDRIARTGVAALPTE---RALALFDSALRRG 3354
QY 176 IEVARP-----RSVIGK-NTVEAMQSGIVYG---FAGQVD---GVVNRMARLADDDPDDV 223
Db 3355 GEVVFPLSINRSALRRAEFVPEVLRGMVRAKLRAAGQAEAAAGPNVVDRLAGRSESD---- 3410
QY 224 TVIATGGLAPMVLGESSVI 242
Db 3411 ---QVAGLAELVRSAAA 3426

RESULT 15
US-08-886-886-13
Sequence 13, Application US/08886886
Patent No. 6107068
GENERAL INFORMATION:
APPLICANT: Katz, Leonard
APPLICANT: Delcardayre, Stephen B.
APPLICANT: Davies, Julian E.
TITLE OF INVENTION: COENZYME A DISULFIDE REDUCTASE,
TITLE OF INVENTION: AND INHIBITORS THEREOF USEFUL AS ANTIMICROBIAL
TITLE OF INVENTION: AGENTS
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/886,886
FILING DATE: 02-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

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;
; ATTORNEY/AGENT INFORMATION:
; NAME: Casuto, Dianne
; REGISTRATION NUMBER: 40,943
; REFERENCE/DOCKET NUMBER: 6016.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-938-3137
; TELEFAX: 847-938-2623
; TELEX:
;
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 549 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
;
US-08-886-886-13
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Query Match      6.3%; Score 84; DB 3; Length 549;
Best Local Similarity 22.7%; Pred. No. 1.1;
Matches 54; Conservative 41; Mismatches 63; Indels 80; Gaps 14;

JY 70 VPSVLHELREVTTRYGDVPAVLVEPGVKGTGPILTD--HPKEV-----GADRIINAV 120
   | : | | | : | | : : | | | | | : | | : | : | : | : | :
Db 89 VITVKHETEILTEHY----DKLILSPGAKPFVPPITGLAEAKNVPSLRNVPDLQIMTAL 144
   | : | | | : | | : | : | : | : | : | : | : | : | : | :
QY 121 AAVELYGGPAIVDFGTATTFDAVSARGEYIGGVIAPGIEISVEALGVKGAQLRKIE--- 177
   | : | | | : | | : | : | : | : | : | : | : | : | : | :
Db 145 -----TPETKRAVVIGAGFI-----GLEMA-ENLQKRGLEVTIVEKAP 181
   | : | | | : | | : | : | : | : | : | : | : | : | : | :
QY 178 -----VARPRSVIGKNTVEAM--QSGIVYGFAGQV-----DGVNRMARELADDPD 221
   | : | | | : | | : | : | : | : | : | : | : | : | : | :
Db 182 HVLPLDEEMAAAFVKAELSKNNVQVITGQSAVAFEEEGQVIRLEDG-----QTLA---S 232
   | : | | | : | | : | : | : | : | : | : | : | : | : | :
QY 222 DVTVIATG-----GLAPMVLGESSVIDEH-----EPWLTLMGLRLVYERNVSR 264
   | : | | | : | | : | : | : | : | : | : | : | : | : | :
Db 233 DLTILSVGVQPENTLAVEAGVATGLRG-GIVVDEHYQTNQPDIIYAVGDVAVVVKQKITQ 289
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Search completed: June 24, 2003, 21:49:15
Job time : 9.74147 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 24, 2003, 22:08:46 ; Search time 12.0821 Seconds
(without alignments)
2373.336 Million cell updates/sec

Title: US-09-813-453A-4
Perfect score: 1343
Sequence: 1 MLLTIDVGNTHVTVLGLFEDGE.....EPWLTLMGLRLVYERNVSRM 265

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 417779 seqs, 108206813 residues
Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :				Published Applications_AA.*	
				1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*	
				2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*	
				3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*	
				4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*	
				5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*	
				6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*	
				7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*	
				8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*	
				9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*	
				10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*	
				11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*	
				12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*	
				13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*	
				14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1343	100.0	265	9	US-09-813-453A-4
2	698.5	52.0	272	9	US-09-813-453A-5
3	694.5	51.7	272	9	US-09-712-363-276
4	663	49.4	258	9	US-09-813-453A-49
5	662	49.3	254	9	US-09-813-453A-47
6	655	48.8	258	9	US-09-813-453A-2
7	643.5	47.9	256	9	US-09-813-453A-55
8	638	47.5	262	9	US-09-813-453A-45
9	629	46.8	255	9	US-09-813-453A-7
10	554.5	41.3	233	9	US-09-813-453A-17
11	527	39.2	258	9	US-09-813-453A-6
12	517	38.5	260	9	US-09-813-453A-51
13	498.5	37.1	250	9	US-09-813-453A-3
14	492.5	36.7	219	9	US-09-813-453A-57
15	409.5	30.5	262	9	US-09-813-453A-8
16	342.5	25.5	246	9	US-09-813-453A-9
17	295	22.0	257	9	US-09-813-453A-53
18	291.5	21.7	273	9	US-09-813-453A-10
19	280	20.8	212	9	US-09-813-453A-59

20	210	15.6	249	9	US-09-813-453A-61	Sequence 61, Appl
21	205.5	15.3	244	9	US-09-813-453A-41	Sequence 41, Appl
22	184	13.7	241	9	US-09-813-453A-63	Sequence 63, Appl
23	181.5	13.5	262	9	US-09-813-453A-11	Sequence 11, Appl
24	180.5	13.4	592	9	US-09-813-453A-22	Sequence 22, Appl
25	179	13.3	460	9	US-09-813-453A-39	Sequence 39, Appl
26	177	13.2	592	9	US-09-813-453A-43	Sequence 43, Appl
27	176	13.1	249	9	US-09-813-453A-70	Sequence 70, Appl
28	174	13.0	257	9	US-09-813-453A-13	Sequence 13, Appl
29	139	10.3	242	9	US-09-813-453A-65	Sequence 65, Appl
30	138.5	10.3	248	9	US-09-813-453A-20	Sequence 20, Appl
31	134	10.0	267	9	US-09-813-453A-15	Sequence 15, Appl
32	128.5	9.6	229	9	US-09-813-453A-12	Sequence 12, Appl
33	95.5	7.1	472	9	US-09-712-363-202	Sequence 202, App
34	92.5	6.9	525	10	US-09-815-242-11952	Sequence 11952, A
35	92	6.9	221	9	US-09-738-626-4878	Sequence 4878, Ap
36	91.5	6.8	1113	9	US-09-738-626-5279	Sequence 5279, Ap
37	91.5	6.8	1113	9	US-10-284-138-3	Sequence 3, Appli
38	91.5	6.8	1113	9	US-10-284-334-3	Sequence 3, Appli
39	91.5	6.8	1113	10	US-09-836-470B-3	Sequence 3, Appli
40	90	6.7	379	9	US-09-975-139-8	Sequence 8, Appli
41	90	6.7	937	9	US-10-126-927-66	Sequence 66, Appl
42	90	6.7	937	9	US-10-126-931A-66	Sequence 66, Appl
43	89.5	6.7	794	10	US-09-815-242-5697	Sequence 5697, Ap
44	89.5	6.7	802	10	US-09-815-242-12668	Sequence 12668, A
45	88.5	6.6	1446	9	US-10-166-087-44	Sequence 44, Appl

ALIGNMENTS

RESULT 1
US-09-813-453A-4
; Sequence 4, Application US/09813453A
; Patent NO. US20020168681A1
; GENERAL INFORMATION:
; APPLICANT: Yocum, R. Rogers
; APPLICANT: Patterson, Thomas A.
; TITLE OF INVENTION: MICROORGANISMS AND ASSAYS FOR THE IDENTIFICATION OF
; TITLE OF INVENTION: ANTIBIOTICS
; FILE REFERENCE: OGZ-001
; CURRENT APPLICATION NUMBER: US/09/813,453A
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/227,860
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 09/667,569
; PRIOR FILING DATE: 2000-09-21
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Streptomyces coelicolor
US-09-813-453A-4

Query Match		100.0%;	Score 1343;	DB 9;	Length 265;
Best Local Similarity		100.0%;	Pred. No. 1.4e-109;		
Matches 265;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MLLTIDVGNTHVTVLGLDGEDIVEHWRISTDSRRRTADELAVLLQGLMGHPLLGDELGDG	60		
Db	1	MLLTIDVGNTHVTVLGLDGEDIVEHWRISTDSRRRTADELAVLLQGLMGHPLLGDELGDG	60		
QY	61	IDGIAICATVPSVLHELREVTTRYGDPVAVLVEPGVKTGVPILTDHPKEVGADRIINAV	120		
Db	61	IDGIAICATVPSVLHELREVTTRYGDPVAVLVEPGVKTGVPILTDHPKEVGADRIINAV	120		
QY	121	AAVELYGGPAIVVDFGTATTFDAVSARGEYIGGVIAPIGTEISVEALGVKGQALRKIEVAR	180		
Db	121	AAVELYGGPAIVVDFGTATTFDAVSARGEYIGGVIAPIGTEISVEALGVKGQALRKIEVAR	180		
QY	181	PRSVIGKNTVEAMQSGIYVGFAGQVDGVNRMARELADDDVTVIATGGLAPMVLGESS	240		

Matches	129;	Conservative	58;	Mismatches	69;	Indels	8;	Gaps	5;
QY	1	MLLTIDVGNTHTVLGLFDGEDIVEHWRISTDSRRTADELAVLLQGLGMHPLLGLDELGDG	60						
Db	1	MIFVLDVGNNTNTVLGVYDGDDELKHHWRIETSRKTEDEICMMIKALLN-H--VGLQFSD-	56						
QY	61	IDGIAICATVPSPVLHRELREVTRRYYGDVPAVLVEPGVKTGPVILTDHPKEVGADRIINAV	120						
Db	57	IRGIIISVVPPIMFALERMCCLKYF-HIKPLIVPGIKTGLDIKYDNPREVGAADRIINAV	115						
QY	121	AAVELYGGPAIVVDFGATTFDAVSARGEYIGGVIAPGIEISVEALGVKGAQLRKIEVAR	180						
Db	116	AGIHLYGSPLIIVDFGATTCYINEHKQYMGGAIAPIGMISTEALFARAAKLPRIEVAR	175						
QY	181	PRSVIGKNTVEAMQSGIYVGFAGQVDGVVNRMARLADDPDDVTVIATGGLAPMVLGESS	240						
Db	176	PDDIIGKNTVSAMQAGILYGVVGQVEGIVSRMKAKSKIPP---KVIATGGLAPLIASESD	232						
QY	241	VIDEHEPWLTLMLGLRLVYERNVSR	264						
b	233	IIDVVDPFLLTGLKLLYEKNTK	256						

RESULT 5
US-09-813-453A-47
; Sequence 47, Application US/09813453A
; Patent No. US20020168681A1
; GENERAL INFORMATION:
; APPLICANT: Yocum, R. Rogers
; APPLICANT: Patterson, Thomas A.
; TITLE OF INVENTION: MICROORGANISMS AND ASSAYS FOR THE IDENTIFICATION OF
; TITLE OF INVENTION: ANTIBIOTICS
; FILE REFERENCE: OGZ-001
; CURRENT APPLICATION NUMBER: US/09/813,453A
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/227,860
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 09/667,569
; PRIOR FILING DATE: 2000-09-21
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Bacillus halodurans
US-09-813-453A-47

Query Match	49.3%;	Score 662;	DB 9;	Length 254;
Best Local Similarity	49.8%;	Pred. No. 3.4e-50;		
Matches 132;	Conservative 55;	Mismatches 64;	Indels 14;	Gaps 4;
QY	1	MLLTIDVGNTHVGLFGEDIVEHWRISTDSRRRTADELAVLLQGLGMHPLLGLDELG--	58	
Db	1	MILVIDVGNNTVGLGVYQDETIVHHWRLATSRQKTEDEYAMTVRSLF-----DHAGLQ	53	
QY	59	-DGIDGIAICAFVPSVLHELREVTRRYYGDVPAVLVPEPGVKTGVPILTDHPKEVGADRII	117	
Db	54	FQDIDGIVISSVPPMMFSLQMCCKYFHVTP-MIIGPGIKTGLNIKYDNPKEVGADRIV	112	
QY	118	NAVAAEVLYGGPAIVVDFTATTFDVARSARGEYIGGVIAPGIEISVEALGVKGAQLRKIE	177	
Db	113	NAVAAEVLYGGPAIVVDFTATTYCLINEKKQYAGGVIAPGIMISTEALYHRASKLPRIE	172	
QY	178	VARPSRVIGKNTVEAMQSGIVYGFAGQVDGVVNRMARLADDDPDDVTVIATGGGLAPMVLG	237	
Db	173	IAKPKQVVGTNTIDSMQSGIFGYVSVQVDGVVKRMKAQAESEP---KVIAATGGGLAKLIGT	229	
QY	238	ESSVIDEHEPWLTMGLRLVYERNV	262	
Db	230	ESETIDVIDSFLLTKGLQLIYKKNV	254	

RESULT 6

US-09-813-453A-2
; Sequence 2, Application US/09813453A
; Patent No. US20020168681a1
; GENERAL INFORMATION:
; APPLICANT: Yocum, R. Rogers
; APPLICANT: Patterson, Thomas A.
; TITLE OF INVENTION: MICROORGANISMS AND ASSAYS FOR THE IDENTIFICATION OF
; TITLE OF INVENTION: ANTIBIOTICS
; FILE REFERENCE: OGZ-001
; CURRENT APPLICATION NUMBER: US/09/813,453A
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/227,860
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 09/667,569
; PRIOR FILING DATE: 2000-09-21
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 2
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-09-813-453A-2

Query Match	48.8%;	Score	655;	DB	9;	Length	258;
Best Local Similarity	51.0%;	Pred. NO.	1.4e-49;				
Matches	133;	Conservative	46;	Mismatches	74;	Indels	8;
						Gaps	3;
QY	1	MLLTIDVGNTHTVLGLFDGEDIVEHWRISTDSRRTADELAVLLQGLMGHPLLGLDELGDG	60				
Db	1	LLLVIDVGNTHTVLGVYHDGKLEYHWRIETSRHKTEDEFGMILRSLFDHSGLMFEQ----	56				
QY	61	IDGIAICATVPSVLHLELREVTRRYYGDVPAVLVEPGVKTVGPILTDHPKEVGADRIINAV	120				
Db	57	IDGIIISVVPPIMFALERMCTKYFHIEPQI-VGFGMKTGLNIKYDNPKEVGADRIINAV	115				
QY	121	AAVELYGGPAVVDFGTATTFDAVSARGEYIGGVYIAPGIEISVEALGVKGAQLRKIEVAR	180				
Db	116	AAIHLVGNPLVVDFGTATTCYIIDENKQYMGGAAPGITISTEALYSRAAKLPRIETR	175				
QY	181	PRSVIGKNTVEAMQSGIVYGFAGQVDGVVNRMARLADDDPDDVTVIATGGLAPMVLGESS	240				
Db	176	PDNIIGKNTVSAMQSGILFYGVQVEGIVKRMKWA---KQDLKVIATGGLAPLIANESD	232				
QY	241	VIDEHEPWLTLMGLRLVYERN	261				
Db	233	CIDIVDPFLTTLKGLLEIYERN	253				

RESULT 7
US-09-813-453A-55
; Sequence 55, Application US/09813453A
; Patent No. US20020168681A1
; GENERAL INFORMATION:
; APPLICANT: Yocum, R. Rogers
; APPLICANT: Patterson, Thomas A.
; TITLE OF INVENTION: MICROORGANISMS AND ASSAYS FOR THE IDENTIFICATION OF
; TITLE OF INVENTION: ANTIBIOTICS
; FILE REFERENCE: OGZ-001
; CURRENT APPLICATION NUMBER: US/09/813,453A
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/227,860
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 09/667,569
; PRIOR FILING DATE: 2000-09-21
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 55
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Clostridium difficile
US-09-813-453A-55

Query Match	47.98;	Score 643.5;	DB 9;	Length 256;
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GenCore version 5.1.6
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*OM protein - protein search, using sw model

Run on: June 24, 2003, 21:46:39 ; Search time 29.4306 Seconds
(without alignments)
1177.181 Million cell updates/sec

Title: US-09-813-453A-51
Perfect score: 1299
Sequence: 1 MLLAIEQGNTNTMFAIHG.....SDLTIRGLLEIYRNTIAES 260

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1299	100.0	260	AAU91173	Pantothenate kinas
2	658	50.7	258	AAU91153	Rhodobacter capsul
3	598	46.0	254	AAU91171	Pantothenate kinas
4	577	44.4	258	AAU01243	B. subtilis novel
5	577	44.4	258	AAU91149	Bacillus subtilis
6	575	44.3	258	AAU91172	Pantothenate kinas
7	566	43.6	262	AAU91170	Pantothenate kinas
8	561	43.2	255	AAU91154	Geobacter sulfurre
9	523.5	40.3	256	AAU91175	Pantothenate kinas
10	523	40.3	259	ABB47661	Listeria monocytog

11	517	39.8	265	23	AAU911151	Streptomyces coeli
12	492	37.9	233	23	AAU911163	Pantothenate kinas
13	478	36.8	219	23	AAU911176	Pantothenate kinas
14	460.5	35.5	250	23	AAU911150	Clostridium acetob
15	396.5	30.5	262	23	AAU911155	Deinococcus radiop
16	382.5	29.4	272	23	AAU911152	Mycobacterium tube
17	378.5	29.1	272	22	AAG81225	Mycobacterium tube
18	359.5	27.7	246	23	AAU911156	Thermotoga maritim
19	337.5	26.0	273	23	AAU911157	Treponema pallidum
20	307.5	23.7	212	23	AAU911177	Pantothenate kinas
21	261	20.1	257	23	AAU911174	Pantothenate kinas
22	227	17.5	241	23	AAU911179	Pantothenate kinas
23	198	15.2	244	23	AAU911168	Pantothenate kinas
24	189.5	14.6	262	23	AAU911158	Borrelia burgdorfe
25	185	14.2	455	20	AAU38617	Neisseria gonorrh
26	185	14.2	455	21	AAU74908	Neisseria gonorrh
27	185	14.2	460	23	AAU911167	Pantothenate kinas
28	185	14.2	592	20	AAU38618	Neisseria gonorrh
29	185	14.2	592	21	AAU74911	Neisseria gonorrh
30	175	13.5	455	21	AAU74910	Neisseria meningit
31	175	13.5	592	20	AAU38616	Neisseria meningit
32	175	13.5	592	21	AAU74913	Neisseria meningit
33	175	13.5	592	23	AAU911166	Pantothenate kinas
34	173.5	13.4	389	21	AAU74909	Neisseria meningit
35	172	13.2	592	20	AAU38615	Neisseria meningit
36	172	13.2	592	21	AAU74912	Neisseria meningit
37	172	13.2	592	23	AAU911169	Pantothenate kinas
38	160	12.3	248	23	AAU911164	Pantothenate kinas
39	153.5	11.8	249	23	AAU911178	Pantothenate kinas
40	147	11.3	257	23	AAU911160	Synechocystis pant
41	141	10.9	249	23	AAU911182	Pantothenate kinas
42	140.5	10.8	242	23	AAU911180	Pantothenate kinas
43	134.5	10.4	267	23	AAU911162	Bordetella pertussis
44	125.5	9.7	229	23	AAU911159	Aquifex aeolicus p
45	116.5	9.0	189	20	AAU38614	Neisseria meningit

ALIGNMENTS

RESULT 1
AAU91173
ID AAU91173 standard; Protein; 260 AA.
XX
AC AAU91173;
XX
DT 05-JUN-2002 (first entry)
XX
DE Pantothenate kinase (Coax) #11.
XX
KW Pantothenate kinase; Coax; antibiotic; antimicrobial;
KW pantothenate kinase modulator; coenzyme A; bactericidal compound.
XX
OS Caulobacter crescentus.
XX
PN WO200216601-A2.
XX
PD 28-FEB-2002.
XX
PF 24-AUG-2001; 2001WO-US26531.
XX
PR 24-AUG-2000; 2000US-227860P.
PR 20-MAR-2001; 2001US-0813453.
XX
PA (OMNI-) OMNIGENE BIOPRODUCTS INC.
XX
PI Yocum RR, Patterson TA;
XX
DR WPI; 2002-269358/31.
DR N-PSDB; ABK54194.
XX
PT Identifying potential antibiotic or antimicrobial agent, comprises contacting composition comprising pantothenate kinase (Coax) protein

PT with test compound and identifying inhibitor of the Coax protein -
XX
PS Claim 10; Page 102-103; 128pp; English.
XX
CC The invention describes assays for identifying a (potential) antibiotic
CC comprising contacting an assay composition comprising a pantothenate
CC kinase (Coax) protein with a test compound, and determining the ability
CC of the test compound to inhibit the activity of the Coax protein, an
CC essential enzyme for the production of coenzyme A. Coax protein is a
CC valuable target for identifying bactericidal compounds. Coax modulating
CC agents can be used in an infectious animal model to determine the
CC efficacy, toxicity, or side effects of treatment with such an agent. This
CC is the amino acid sequence of a pantothenate kinase (Coax) protein
CC described in the invention.

XX
SQ Sequence 260 AA;
Query Match 100.0%; Score 1299; DB 23; Length 260;
Best Local Similarity 100.0%; Pred. No. 8.3e-133;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MLLAIEQGNNTMFAIHGASWVAQWRSATESRTRTADEYVWVLSQLLSMQGLGFRAIDAV 60
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1 MLLAIEQGNNTMFAIHGASWVAQWRSATESRTRTADEYVWVLSQLLSMQGLGFRAIDAV 60
|||||
QY 61 IISVVVQSIFNLRNLSRRYFNVPLVIGENAKLGIDVRIEKPSEAGADRLVNAIGAAMV 120
|||||
Db 61 IISVVVQSIFNLRNLSRRYFNVPLVIGENAKLGIDVRIEKPSEAGADRLVNAIGAAMV 120
|||||
QY 121 YPGPLVVIDSGTATTFDIVAADGAFEGGIIAPGINLSMQALHEAAKLPRIAIOQPAGNR 180
|||||
Db 121 YPGPLVVIDSGTATTFDIVAADGAFEGGIIAPGINLSMQALHEAAKLPRIAIOQPAGNR 180
|||||
QY 181 IVGTDVTSAMQSGVFWGYISLIEGLVARIKAERGEPMVTVIATGGVASLFEGATDSIDHFD 240
|||||
Db 181 IVGTDVTSAMQSGVFWGYISLIEGLVARIKAERGEPMVTVIATGGVASLFEGATDSIDHFD 240
|||||
QY 241 SDLTIRGLLEIYRNTIAES 260
|||||
Db 241 SDLTIRGLLEIYRNTIAES 260
|||||

RESULT 2
AAU91153
ID AAU91153 standard; Protein; 258 AA.
XX
AC AAU91153;
XX
DT 05-JUN-2002 (first entry)
XX
KW Rhodobacter capsulatus pantothenate kinase Coax.
KW Pantothenate kinase; Coax; antibiotic; antimicrobial;
KW pantothenate kinase modulator; coenzyme A; bactericidal compound.
OS Rhodobacter capsulatus.
XX WO200216601-A2.
PN
PD 28-FEB-2002.
XX
PF 24-AUG-2001; 2001WO-US26531.
XX
PR 24-AUG-2000; 2000US-227860P.
PR 20-MAR-2001; 2001US-0813453.
XX
PA (OMNI-) OMNIGENE BIOPRODUCTS INC.
XX
PI Yocum RR, Patterson TA;
XX
DR WPI; 2002-269358/31.
XX
PT Identifying potential antibiotic or antimicrobial agent, comprises

PT contacting composition comprising pantothenate kinase (Coax) protein
PT with test compound and identifying inhibitor of the Coax protein -
XX
PS Claim 10; Page 71-72; 128pp; English.
XX
CC The invention describes assays for identifying a (potential) antibiotic
CC comprising contacting an assay composition comprising a pantothenate
CC kinase (Coax) protein with a test compound, and determining the ability
CC of the test compound to inhibit the activity of the Coax protein, an
CC essential enzyme for the production of coenzyme A. Coax protein is a
CC valuable target for identifying bactericidal compounds. Coax modulating
CC agents can be used in an infectious animal model to determine the
CC efficacy, toxicity, or side effects of treatment with such an agent. This
CC is the amino acid sequence of a pantothenate kinase (Coax) protein
CC described in the invention.

XX
SQ Sequence 258 AA;
Query Match 50.7%; Score 658; DB 23; Length 258;
Best Local Similarity 50.8%; Pred. No. 4.9e-63;
Matches 130; Conservative 48; Mismatches 74; Indels 4; Gaps 3;

QY 1 MLLAIEQGNNTMFAIHGASWVAQWRSATESRTRTADEYVWVLSQLLSMQGLGFRAIDAV 60
|||||
Db 1 MLLCIDCGNTNTVFSVWDGTDFAAATWRIATDHRRTADEYFVWLNTLMQLKQLGR-ISEA 59
|||||
QY 61 IISVVVQSIFNLRNLSRRYFNVPLVIGE-NAKLGIDVRIEKPSEAGADRLVNAIGAAM 119
|||||
Db 60 IISSTAPRVVFNLRVLCNRYFDCRPYVVGKPGCELPVAPRVDPGTTVGPDRLVNTVAGYD 119
|||||
QY 120 YPGPLVVIDSGTATTFDIVAADGAFEGGIIAPGINLSMQALHEAAKLPRIAIOQPAGN 179
: |||
Db 120 RHGGDLIVDFGTATTFDVVPDGYIGGVIAPIGVNLSLEALHMAAALPHVDVTKPQG- 178
|||||
QY 180 RIVGTDVTSAMQSGVFWGYISLIEGLVARIKAERGEPMVTVIATGGVASLFEGATDSIDHF 239
: |||
Db 179 -VIGTNTVACIQSGVYWGVIIGLVGIVRQIRMERDRPMKVIATGGLASLFDLGLDFDKV 237
|||||
QY 240 DSDLTIRGLLEIYRNRN 255
: |||
Db 238 EDDLTMHGLRLIFDYN 253
|||||

RESULT 3
AAU91171
ID AAU91171 standard; Protein; 254 AA.
XX
AC AAU91171;
XX
DT 05-JUN-2002 (first entry)
XX
DE Pantothenate kinase (Coax) #9.
XX Pantothenate kinase; Coax; antibiotic; antimicrobial;
KW pantothenate kinase modulator; coenzyme A; bactericidal compound.
XX Bacillus halodurans.
XX WO200216601-A2.
PN
PD 28-FEB-2002.
XX
PF 24-AUG-2001; 2001WO-US26531.
XX
PR 24-AUG-2000; 2000US-227860P.
PR 20-MAR-2001; 2001US-0813453.
XX
PA (OMNI-) OMNIGENE BIOPRODUCTS INC.
XX
PI Yocum RR, Patterson TA;
XX
DR WPI; 2002-269358/31.
DR N-PSDB; ABK54192.

XX Identifying potential antibiotic or antimicrobial agent, comprises
PT contacting composition comprising pantothenate kinase (Coax) protein
PT with test compound and identifying inhibitor of the Coax protein
XX
PS Claim 10; Page 100; 128pp; English.
XX
CC The invention describes assays for identifying a (potential) antibiotic
CC comprising contacting an assay composition comprising a pantothenate
CC kinase (Coax) protein with a test compound, and determining the ability
CC of the test compound to inhibit the activity of the Coax protein, an
CC essential enzyme for the production of coenzyme A. Coax protein is a
CC valuable target for identifying bactericidal compounds. Coax modulating
CC agents can be used in an infectious animal model to determine the
CC efficacy, toxicity, or side effects of treatment with such an agent. This
CC is the amino acid sequence of a pantothenate kinase (Coax) protein
CC described in the invention.
XX

SQ Sequence 254 AA;
Query Match 46.0%; Score 598; DB 23; Length 254;
Best Local Similarity 43.9%; Pred. No. 1.6e-56;
Matches 112; Conservative 61; Mismatches 80; Indels 2; Gaps 1;

QY 1 MLLAIEQGNNTMFAIHGASWVAQWRSATESSTRTADEYVWVLSQLLSMQGLGFRAIDAV 60
Db 1 MILVIDGNTNTVLGVYQDETIVHHWRLATSRQKTEDEYAMTVRSLEFDHAGLQFQDIDGI 60
QY 61 IISVVPPQSIFNLNLSRRYFNVEPLVIGENAKLGIDVRIEKPSEAGADRLVNAIGAAMV 120
Db 61 VISSVPPMMFSLQEQMCKKYFHTVPMIIGPGIKTGLNLIKYNPKVEGADRVNAVAIAEL 120
QY 121 YPGPLVVIDSGTATTFDIVAADGAFEGGIIAPGINLSMQALHEAAKLPRIAIPAGNR 180
Db 121 YGYPVAVVDFGTATYCLINEKKQYAGGVIAPIGIMISTEALYHRASKLPRIEIAKP--KQ 178
QY 181 IVGTDVTSAMQSGVFWGYISLIEGLVARIKAEERGEPTMTVIATGGVASFEGATDSIDHFD 240
Db 179 VVGNTIDSMQSGIFYGYVSQVDGVVVRMKQAQAESEPKVIATGGLAKLIGTSETIDVID 238
QY 241 SDLTIRGLLEIYRRN 255
Db 239 SFLTGLGLLIYKKN 253

RESULT 4
AAU01243
D AAU01243 standard; Protein; 258 AA.
X
AC AAU01243;

XX 18-JUL-2001 (first entry)
DT
XX B. subtilis novel pantothenate kinase encoded by the gene coax.
DE
XX Pantothenate kinase; coax; pantothenate biosynthesis; vitamin B5;
KW nutritional supplement; panto-compound; pantoate.
XX
OS Bacillus subtilis.

XX WO200121772-A2.
PN
XX 29-MAR-2001.
PD
XX 21-SEP-2000; 2000WO-US255993.

XX 21-SEP-1999; 99US-0400494.
PR
XX 07-JUN-2000; 2000US-0210072.
PR
XX 28-JUL-2000; 2000US-0221836.
PR
XX 24-AUG-2000; 2000US-0227860.

XX (OMNI-) OMNIGENE BIOPRODUCTS.
PA
XX

PI Yocum RR, Patterson TA, Hermann T, Pero JG;
XX
DR WPI; 2001-218644/22.
DR N-PSDB; AAS00984.
XX
PT New recombinant microorganism which overexpress a Bacillus subtilis
PT pantothenate biosynthetic enzyme, useful for the high yield production
PT of panto-compounds such as pantothenate and pantoate
XX
PS Example 14; Fig 23; 292pp; English.

XX The sequence represents a novel B. subtilis pantothenate kinase (encoded
CC by gene coax), an enzyme of the pantothenate biosynthetic pathway.
CC Pantothenate, also known as vitamin B5, is used as a nutritional
CC supplement in mammals and humans. The invention concerns methods of
CC producing recombinant microorganisms overexpressing at least one Bacillus
CC subtilis pantothenate biosynthetic enzyme. The microorganisms and methods
CC of producing them are useful for producing a panto-compound such as
CC pantothenate or pantoate, which is a nutritional requirement for
CC livestock and humans. The methods are also useful for the identification
CC of pantothenate kinase modulators. Panto-compounds are produced at a
CC significantly higher yield than prior art methods and can be produced
CC independent of the need to feed precursors which decreases expense.
XX

SQ Sequence 258 AA;
Query Match 44.4%; Score 577; DB 22; Length 258;
Best Local Similarity 44.4%; Pred. No. 3.2e-54;
Matches 114; Conservative 50; Mismatches 91; Indels 2; Gaps 1;

QY 1 MLLAIEQGNNTMFAIHGASWVAQWRSATESSTRTADEYVWVLSQLLSMQGLGFRAIDAV 60
Db 1 LLLVIDGNTNTVLGVYHDKLEYHWRITSRHKTEDEFGMILRSLFDHSGLMFEQIDGI 60
QY 61 IISVVPPQSIFNLNLSRRYFNVEPLVIGENAKLGIDVRIEKPSEAGADRLVNAIGAAMV 120
Db 61 IISVVPPIMEFALERMCTKYFHIEPQIVGPMKMTGLNLIKYNPKVEGADRVNAVAIAHL 120
QY 121 YPGPLVVIDSGTATTFDIVAADGAFEGGIIAPGINLSMQALHEAAKLPRIAIPAGNR 180
Db 121 YGNPLIVVDFGTATYCYIDENKQYMGGAIPGITISTEALYSRAAKLPRIETRP--DN 178
QY 181 IVGTDVTSAMQSGVFWGYISLIEGLVARIKAEERGEPTMTVIATGGVASFEGATDSIDHFD 240
Db 179 IIGKNTVSAMQSGILFGYVGVQVEGIVKRMKQAKQDLKVIATGGLAPLIANESDCIDIVD 238
QY 241 SDLTIRGLLEIYRRNTI 257
Db 239 PFLTGLGLLIYERNRV 255

RESULT 5
AAU91149
ID AAU91149 standard; Protein; 258 AA.
XX
AC AAU91149;

XX 05-JUN-2002 (first entry)
DT
XX Bacillus subtilis pantothenate kinase Coax.

XX Pantothenate kinase; Coax; antibiotic; antimicrobial;
KW pantothenate kinase modulator; coenzyme A; bactericidal compound.
XX
OS Bacillus subtilis.

XX WO200216601-A2.
PN
XX 28-FEB-2002.
PD
XX 24-AUG-2001; 2001WO-US26531.

XX 24-AUG-2000; 2000US-227860P.
PR

PR 20-MAR-2001; 2001US-0813453.
XX (OMNI-) OMNIGENE BIOPRODUCTS INC.
PA Yocum RR, Patterson TA;
PI WPI; 2002-269358/31.
XX N-PSDB; ABK54168.

Identifying potential antibiotic or antimicrobial agent, comprises contacting composition comprising pantothenate kinase (Coax) protein with test compound and identifying inhibitor of the Coax protein -
Claim 10; Page 67-68; 128pp; English.

The invention describes assays for identifying a (potential) antibiotic comprising contacting an assay composition comprising a pantothenate kinase (Coax) protein with a test compound, and determining the ability of the test compound to inhibit the activity of the Coax protein, an essential enzyme for the production of coenzyme A. Coax protein is a valuable target for identifying bactericidal compounds. Coax modulating agents can be used in an infectious animal model to determine the efficacy, toxicity, or side effects of treatment with such an agent. This is the amino acid sequence of a pantothenate kinase (Coax) protein described in the invention.

Sequence 258 AA;

Query Match 44.4%; Score 577; DB 23; Length 258;
Best Local Similarity 44.4%; Pred. No. 3.2e-54;
Matches 114; Conservative 50; Mismatches 91; Indels 2; Gaps 1;

QY 1 MLLAIEQGNNTMFAIHGASWVAQWRSATESSTRTADEYVWLSQLLSMQGLGFRAIDAV 60
Db 1 LLLVIDVGNTNTVLGVYHDGKLEYHWRIETSRHKTDEFGMLRSLFDHSGLMFEQIDGI 60
QY 61 IISVVVPQSIFNLRNLSRRYFNVEPLVIGENAKLGIDVRIEKPSEAGADRLVNAIGAAMV 120
Db 61 IISVVPPIMFALERMCTKYFHIEPQIVGPGMKTGLNLIKVDNPKVEGADRIVNAVAIHL 120
QY 121 YGPLVVIDSGTATTFDIVAADGAFEGGIIAPGINLSMQALHEAAKLPRIAIQRPAGNR 180
Db 121 YGNPLIVDFGTATTCYIDENKQYMGGAIAPIGTISTEALYSRAAKLPRIETRP--DN 178
QY 181 IVGDTVSAMQSGVFWGYISLIEGLVARIKAERGEPMVTVIATGGVASLFEGATSDIDHFD 240
Db 179 IIGKNTVSAMQSGILFGYGVQVEGIVKRMKQAKDLKVIATGGLAPLIANESDCIDIVD 238
QY 241 SDLTIRGLLEIYRRNTI 257
239 PFLTGLGLELIYERNV 255

RESULT 6
AAU91172
ID AAU911172 standard; Protein; 258 AA.
XX AAU911172;
AC
XX 05-JUN-2002 (first entry)
XX Pantothenate kinase (Coax) #10.

Pantothenate kinase (Coax) #10.
Pantothenate kinase; Coax; antibiotic; antimicrobial;
pantothenate kinase modulator; coenzyme A; bactericidal compound;
Bacillus stearothermophilus.
WO200216601-A2.
XX 28-FEB-2002.
PD 24-AUG-2001; 2001WO-US26531.
PF

XX 24-AUG-2000; 2000US-227860P.
PR 20-MAR-2001; 2001US-0813453.
XX (OMNI-) OMNIGENE BIOPRODUCTS INC.
PA Yocum RR, Patterson TA;
PI WPI; 2002-269358/31.
XX N-PSDB; ABK54193.

Identifying potential antibiotic or antimicrobial agent, comprises contacting composition comprising pantothenate kinase (Coax) protein with test compound and identifying inhibitor of the Coax protein -
Claim 10; Page 101-102; 128pp; English.

The invention describes assays for identifying a (potential) antibiotic comprising contacting an assay composition comprising a pantothenate kinase (Coax) protein with a test compound, and determining the ability of the test compound to inhibit the activity of the Coax protein, an essential enzyme for the production of coenzyme A. Coax protein is a valuable target for identifying bactericidal compounds. Coax modulating agents can be used in an infectious animal model to determine the efficacy, toxicity, or side effects of treatment with such an agent. This is the amino acid sequence of a pantothenate kinase (Coax) protein described in the invention.

Sequence 258 AA;

Query Match 44.3%; Score 575; DB 23; Length 258;
Best Local Similarity 44.1%; Pred. No. 5.3e-54;
Matches 113; Conservative 52; Mismatches 89; Indels 2; Gaps 1;

QY 1 MLLAIEQGNNTMFAIHGASWVAQWRSATESSTRTADEYVWLSQLLSMQGLGFRAIDAV 60
Db 1 MIFVLDVGNTNTVLGVYDGDDELKHHWRIETSRSKTEDEYGMKIKALLNHVGLQFSDIRGI 60
QY 61 IISVVVPQSIFNLRNLSRRYFNVEPLVIGENAKLGIDVRIEKPSEAGADRLVNAIGAAMV 120
Db 61 IISVVPPIMFALERMCTKYFHIEPQIVGPGMKTGLDIDKYNPREVGADRIVNAVAGIHL 120
QY 121 YGPLVVIDSGTATTFDIVAADGAFEGGIIAPGINLSMQALHEAAKLPRIAIQRPAGNR 180
Db 121 YGSLIIVDFGTATTCYINEHKQYMGGAIAPIGMISTEALFARAALPRIETARP--DD 178
QY 181 IVGDTVSAMQSGVFWGYISLIEGLVARIKAERGEPMVTVIATGGVASLFEGATSDIDHFD 240
Db 179 IIGKNTVSAMQAGILYGVYGVQVEGIVSRMKAKSKIPPVIATGGLAPLIASESDIIDVVD 238
QY 241 SDLTIRGLLEIYRRNT 256
Db 239 PFLTGLKLLYEKNT 254

RESULT 7
AAU911170
ID AAU911170 standard; Protein; 262 AA.
XX AAU911170;
AC
XX 05-JUN-2002 (first entry)

Pantothenate kinase (Coax) #8.
Pantothenate kinase; Coax; antibiotic; antimicrobial;
pantothenate kinase modulator; coenzyme A; bactericidal compound.
Bacillus anthracis.
WO200216601-A2.
XX 28-FEB-2002.
PD

XX 24-AUG-2001; 2001WO-US26531.
XX 24-AUG-2000; 2000US-227860P.
PR 20-MAR-2001; 2001US-0813453.
XX
PA (OMNI-) OMNIGENE BIOPRODUCTS INC.
XX
PI Yocum RR, Patterson TA;
XX
DR WPI; 2002-269358/31.
DR N-PSDB; ABK54191.

XX Identifying potential antibiotic or antimicrobial agent, comprises
XX contacting composition comprising pantothenate kinase (Coax) protein
XX with test compound and identifying inhibitor of the Coax protein -
PS Claim 8; Page 98-99; 128pp; English.

XX The invention describes assays for identifying a (potential) antibiotic
XX comprising contacting an assay composition comprising a pantothenate
XX kinase (Coax) protein with a test compound, and determining the ability
XX of the test compound to inhibit the activity of the Coax protein, an
XX essential enzyme for the production of coenzyme A. Coax protein is a
XX valuable target for identifying bactericidal compounds. Coax modulating
XX agents can be used in an infectious animal model to determine the
XX efficacy, toxicity, or side effects of treatment with such an agent. This
XX is the amino acid sequence of a pantothenate kinase (Coax) protein
XX described in the invention.

SQ Sequence 262 AA;

Query Match 43.6%; Score 566; DB 23; Length 262;
Best Local Similarity 42.0%; Pred. No. 5.2e-53;
Matches 107; Conservative 55; Mismatches 91; Indels 2; Gaps 1;

QY 1 MLLAIEQGNNTMFAIHDGASWVAQWRSATESTRTADEYVVWLSQLLSMQGLGFRAIDAV 60
Db 1 MIFVLDVGNNTNAVILGVFEEGELRQHWRMETDRHKTEDEYGLVKQLLEHEGLSFEDVKGI 60
QY 61 IISVVVPQSIFNLNLSRRYFNVEPLVIGENAKLGIDVRIEKPSEAGADRLVNAIGAAMV 120
Db 61 IVSSVPPIMPALERMCEKYFKIKPLVVGPGIKTGLNIKYENPREVGADRIVNAVAGIHL 120
QY 121 YGPLVVIDSGTATFDIVAADGAFEGGIIAPGINLSMQALHEAAKLPRIAIOIPAGNR 180
Db 121 YGSLIIVDFGTATCYINEEKHYMGVITPGIMISAEALYSRAAKLPRIETKPSS-- 178
Y 181 IVGTDVTSAMQSGVFWGYISLIEGLVARIKAERGEPMVTIATGGVASFEGATDSIDHFD 240
Db 179 VVGKNTVSAMQSGILYGVGVQVEGIVKRMKEAKQEPKVIATGGLAKLISEESNVIDVD 238
QY 241 SDLTIRGLLEIYRN 255
Db 239 PFLTGLKGLYMLYRN 253

RESULT 8
AAU91154
ID AAU91154 standard; Protein; 255 AA.
XX
AC AAU91154;

XX 05-JUN-2002 (first entry)
XX Geobacter sulfurreducens pantothenate kinase Coax.
DE
XX Pantothenate kinase; Coax; antibiotic; antimicrobial;
KW pantothenate kinase modulator; coenzyme A; bactericidal compound.
XX Geobacter sulfurreducens.
OS
XX WO200216601-A2.

XX 28-FEB-2002.
XX
PF 24-AUG-2001; 2001WO-US26531.
XX
PR 24-AUG-2000; 2000US-227860P.
PR 20-MAR-2001; 2001US-0813453.
XX
PA (OMNI-) OMNIGENE BIOPRODUCTS INC.
XX
PI Yocum RR, Patterson TA;
XX
DR WPI; 2002-269358/31.

XX Identifying potential antibiotic or antimicrobial agent, comprises
XX contacting composition comprising pantothenate kinase (Coax) protein
XX with test compound and identifying inhibitor of the Coax protein -
PS Claim 10; Page 72-73; 128pp; English.

XX The invention describes assays for identifying a (potential) antibiotic
XX comprising contacting an assay composition comprising a pantothenate
XX kinase (Coax) protein with a test compound, and determining the ability
XX of the test compound to inhibit the activity of the Coax protein, an
XX essential enzyme for the production of coenzyme A. Coax protein is a
XX valuable target for identifying bactericidal compounds. Coax modulating
XX agents can be used in an infectious animal model to determine the
XX efficacy, toxicity, or side effects of treatment with such an agent. This
XX is the amino acid sequence of a pantothenate kinase (Coax) protein
XX described in the invention.

SQ Sequence 255 AA;

Query Match 43.2%; Score 561; DB 23; Length 255;
Best Local Similarity 44.7%; Pred. No. 1.8e-52;
Matches 114; Conservative 50; Mismatches 89; Indels 2; Gaps 1;

QY 1 MLLAIEQGNNTMFAIHDGASWVAQWRSATESTRTADEYVVWLSQLLSMQGLGFRAIDAV 60
Db 1 MLLVIDVGNNTNIVLGIYDGERLVRDWRVSTDKARTTDEYGILINELFRLAGLDQIRAV 60
QY 61 IISVVVPQSIFNLNLSRRYFNVEPLVIGENAKLGIDVRIEKPSEAGADRLVNAIGAAMV 120
Db 61 IISVVVPPLTGVLERLSLGYFGMRPLVVGPGIKTGMPIQYDNPREVGADRIVNAVAGYEK 120
QY 121 YGPLVVIDSGTATFDIVAADGAFEGGIIAPGINLSMQALHEAAKLPRIAIOIPAGNR 180
Db 121 YRTSLIIVDFGTATFDYVNRKGEYCGGAIAPGLVISTEALFQRASKLPRIIDIRPSA-- 178
QY 181 IVGTDVTSAMQSGVFWGYISLIEGLVARIKAERGEPMVTIATGGVASFEGATDSIDHFD 240
Db 179 IIRNTVNSMQAGIYYGVGLVDEIVTRMKAESKDPRIATGGLASLIAPESKTIHAVE 238
QY 241 SDLTIRGLLEIYRN 255
Db 239 EYLTLEGLRILYRN 253

RESULT 9
AAU91175
ID AAU91175 standard; Protein; 256 AA.
XX
AC AAU91175;

XX 05-JUN-2002 (first entry)
XX Pantothenate kinase (Coax) #13.
DE
XX Pantothenate kinase; Coax; antibiotic; antimicrobial;
KW pantothenate kinase modulator; coenzyme A; bactericidal compound.
XX Clostridium difficile.

PN WO200216601-A2.
XX
PD 28-FEB-2002.
XX
PF 24-AUG-2001; 2001WO-US26531.
XX
PR 24-AUG-2000; 2000US-227860P.
PR 20-MAR-2001; 2001US-0813453.
XX
PA (OMNI-) OMNIGENE BIOPRODUCTS INC.
XX
XX Yocum RR, Patterson TA;
PI
XX WPI; 2002-2693358/31.
DR N-PSDB; ABK54196.
XX
PT Identifying potential antibiotic or antimicrobial agent, comprises
PT contacting composition comprising pantothenate kinase (Coax) protein
PT with test compound and identifying inhibitor of the Coax protein -
XX
XX Claim 6; Page 105; 128pp; English.
CC The invention describes assays for identifying a (potential) antibiotic
CC comprising contacting an assay composition comprising a pantothenate
CC kinase (Coax) protein with a test compound, and determining the ability
CC of the test compound to inhibit the activity of the Coax protein, an
CC essential enzyme for the production of coenzyme A. Coax protein is a
CC valuable target for identifying bactericidal compounds. Coax modulating
CC agents can be used in an infectious animal model to determine the
CC efficacy, toxicity, or side effects of treatment with such an agent. This
CC is the amino acid sequence of a pantothenate kinase (Coax) protein
CC described in the invention.
XX
SQ Sequence 256 AA;
Query Match 40.3%; Score 523.5; DB 23; Length 256;
Best Local Similarity 40.6%; Pred. No. 2.1e-48;
Matches 104; Conservative 53; Mismatches 96; Indels 3; Gaps 2;
QY 1 MLLAIEQNTNTMFAIHGASWVAQWRSATSTRTADEYVVWLSQQLSMQGLGFRDAIDAV 60
Db 1 MLLVFDVGNNTMVLGIYKDKLVNRYRIKTDREKTSDEYGLISLNFDDYDNNVNSIDDDV 60
QY 61 IISVVVPSQIFNLRNLSRRYFNVPLVIGENAKLGIDVRIEKPSEAGADRLVNAIGAAMV 120
Db 61 IISVVVPSQIFNLRNLSRRYFNVPLVIGENAKLGIDVRIEKPSEAGADRLVNAIGAAMV 120
QY 121 YPGPLVVDSGTATTFDIVAADGAFEGGIIAPGINLSMQALHEAAKLPRIAIOQPAGNR 180
121 YGAPSLVDFGTATTFCAISEKGEYLGGTIAPGIIKISSEALFQSAKLPRLVELAKP--GM 178
QY 181 IVGDTVVSAMQSGVFWGYISLIEGLVARIKAEKRG-EPMTVIATGGVASLFEATDSIDHF 239
Db 179 TICKSTVSAMQSGIYGYVGLVDKIIISIMKKELNCDVVKVIATGGLAKLIASETKSIDYV 238
QY 240 DSDLTIRGLLEIYRN 255
Db 239 DGFLTLEGLRIYEKN 254
RESULT 10
ABB47661
ID ABB47661 standard; Protein; 259 AA.
XX
AC ABB47661;
XX
DT 05-FEB-2002 (first entry)
XX
DE Listeria monocytogenes protein #365.
XX
KW Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
KW vitamin B12; bacterial infection; disease.
XX

OS Listeria monocytogenes.
XX
PN WO200177335-A2.
XX
PD 18-OCT-2001.
XX
PF 11-APR-2001; 2001WO-FR01118.
XX
PR 11-APR-2000; 2000FR-0004629.
XX
PA (INSP) INST PASTEUR.
XX
XX Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P;
PI Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P;
PI Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;
PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L;
PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
PI Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
PI Rose M, Voss H;
XX
DR WPI; 2002-010914/01.
XX
PT Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
PT and prevention of Listeria and related bacterial infections, and
PT related polypeptides -
XX
PS Claim 6; SEQ ID No 366; 192pp; French.
XX
CC The present invention relates to the genome sequence of Listeria
CC monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
CC it are useful for selecting probes and primers for detecting genes in L.
CC monocytogenes and related organisms, and for studying genetic
CC polymorphisms and other genomes. The present sequence is a protein
CC encoded by the genome sequence of the present invention. Proteins
CC expressed from the genome sequence are useful for raising specific
CC antibodies, identification of L. monocytogenes and related organisms, and
CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin
CC B12. The genome sequence and proteins encoded by it are also useful for
CC selecting compounds that regulate gene expression and cell replication
CC and modulate L. monocytogenes-related diseases. In addition, the genome
CC sequence and proteins encoded by it are useful in pharmaceutical and
CC vaccines compositions for the treatment or prevention of infections by L.
CC monocytogenes and related organisms.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 259 AA;
Query Match 40.3%; Score 523; DB 23; Length 259;
Best Local Similarity 39.2%; Pred. No. 2.5e-48;
Matches 100; Conservative 59; Mismatches 94; Indels 2; Gaps 1;
QY 1 MLLAIEQNTNTMFAIHGASWVAQWRSATSTRTADEYVVWLSQQLSMQGLGFRDAIDAV 60
Db 1 MILVIDVGNNTCTVGYEKQKLLKHWRMTTDRHRTSDELGMTVLNFFSYANLTPSDIQGI 60
QY 61 IISVVVPSQIFNLRNLSRRYFNVPLVIGENAKLGIDVRIEKPSEAGADRLVNAIGAAMV 120
Db 61 IISVVVPSQIFNLRNLSRRYFNVPLVIGENAKLGIDVRIEKPSEAGADRLVNAIGAAMV 120
QY 121 YPGPLVVDSGTATTFDIVAADGAFEGGIIAPGINLSMQALHEAAKLPRIAIOQPAGNR 180
Db 121 YGTPVIVDFGTATTCYIDESGVYQGGAIAPGIMISTEALYNRAKLPVDAIE--SSQ 178
QY 181 IVGDTVVSAMQSGVFWGYISLIEGLVARIKAEKRG-EPMTVIATGGVASLFEATDSIDHF 240
Db 179 IIGKSTVSSMQAGIFYGVGQCEGIIAEMKKQSNASPVVATGGLARMIKSSAVDILD 238
QY 241 SDLTIRGLLEIYRN 255
Db 239 PFLTGLLEIYRN 253


```
RESULT 13
AAU91176
ID AAU91176 standard; Protein; 219 AA.
XX
AC AAU91176;
XX
DT 05-JUN-2002 (first entry)
XX
DE Dehalococcoides ethenogenes.
XX
KW Pantothenate kinase (Coax) #14.
KW Pantothenate kinase; Coax; antibiotic; antimicrobial;
KW pantothenate kinase modulator; coenzyme A; bactericidal compound.
XX
OS Dehalococcoides ethenogenes.
XX
PN WO200216601-A2.
XX
PD 28-FEB-2002.
XX
PF 24-AUG-2001; 2001WO-US26531.
PR 24-AUG-2000; 2000US-227860P.
PR 20-MAR-2001; 2001US-0813453.
XX
PA (OMNI-) OMNIGENE BIOPRODUCTS INC.
XX
PI Yocum RR, Patterson TA;
XX
DR WPI; 2002-269358/31.
DR N-PSDB; ABK54197.
XX
PT Identifying potential antibiotic or antimicrobial agent, comprises
PT contacting composition comprising pantothenate kinase (Coax) protein
PT with test compound and identifying inhibitor of the Coax protein.
XX
PS Claim 10; Page 106-107; 128pp; English.
XX
CC The invention describes assays for identifying a (potential) antibiotic
CC comprising contacting an assay composition comprising a pantothenate
CC kinase (Coax) protein with a test compound, and determining the ability
CC of the test compound to inhibit the activity of the Coax protein, an
CC essential enzyme for the production of coenzyme A. Coax protein is a
CC valuable target for identifying bactericidal compounds. Coax modulating
CC agents can be used in an infectious animal model to determine the
CC efficacy, toxicity, or side effects of treatment with such an agent. This
CC is the amino acid sequence of a pantothenate kinase (Coax) protein
CC described in the invention.
XX
Sequence 219 AA;
Query Match 36.8%; Score 478; DB 23; Length 219;
Best Local Similarity 44.9%; Pred. No. 1.5e-43;
Matches 96; Conservative 41; Mismatches 75; Indels 2; Gaps 1;
QY 2 LLAIEQGNNTMTFAIHDGASWVAQWRSATESRTRADEYVYVWLSQGLGFRDAVI 61
Db 5 LVAVDIGNTSVNIGIFEGEKLKLANWHILGSAQRMADAYASLLGLLQHAGIHPEELNRVI 64
QY 62 ISSVVPQSIFNLRNLSRRYFNVEPLVIGENAKLGIDVRIEKPSEAGADRLVNAIGAAMVY 121
Db 65 MCSVVPPLTTTFEEVFKSYFKAAPLVVVGAGIKSGVKVRMDNPREVGADRIVNAARVLY 124
QY 122 PGLVVIDSGTATTFDIVAADGAFEGGIIAPGINLSMQALHEAAKLPRIAIQRPAGNRI 181
Db 125 PGACIIVDMGTATTFDTLSEGGAYIGGAIAPGIATSAQAIAETSKLPKIEIRPA--KV 182
QY 182 VGTDTVSAMQSGVFWGYISLIEGLVARIKAEERGE 215
Db 183 IGSNTVSAMQSGIYFGYIGLVEELVRRIQTELGO 216
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RESULT 14

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AAU91150
ID AAU91150 standard; Protein; 250 AA.
XX
AC AAU91150;
XX
DT 05-JUN-2002 (first entry)
XX
DE Clostridium acetobutylicum pantothenate kinase Coax.
XX
KW Pantothenate kinase; Coax; antibiotic; antimicrobial;
KW pantothenate kinase modulator; coenzyme A; bactericidal compound.
XX
OS Clostridium acetobutylicum.
XX
PN WO200216601-A2.
XX
PD 28-FEB-2002.
XX
PF 24-AUG-2001; 2001WO-US26531.
PR 24-AUG-2000; 2000US-227860P.
PR 20-MAR-2001; 2001US-0813453.
XX
PA (OMNI-) OMNIGENE BIOPRODUCTS INC.
XX
PI Yocum RR, Patterson TA;
XX
DR WPI; 2002-269358/31.
XX
PT Identifying potential antibiotic or antimicrobial agent, comprises
PT contacting composition comprising pantothenate kinase (Coax) protein
PT with test compound and identifying inhibitor of the Coax protein.
XX
PS Claim 10; Page 68-69; 128pp; English.
XX
CC The invention describes assays for identifying a (potential) antibiotic
CC comprising contacting an assay composition comprising a pantothenate
CC kinase (Coax) protein with a test compound, and determining the ability
CC of the test compound to inhibit the activity of the Coax protein, an
CC essential enzyme for the production of coenzyme A. Coax protein is a
CC valuable target for identifying bactericidal compounds. Coax modulating
CC agents can be used in an infectious animal model to determine the
CC efficacy, toxicity, or side effects of treatment with such an agent. This
CC is the amino acid sequence of a pantothenate kinase (Coax) protein
CC described in the invention.
XX
Sequence 250 AA;
Query Match 35.5%; Score 460.5; DB 23; Length 250;
Best Local Similarity 39.5%; Pred. No. 1.5e-41;
Matches 92; Conservative 53; Mismatches 81; Indels 7; Gaps 2;
QY 1 MLLAIEQGNNTMTFAIHDGASWVAQWRSATESRTRADEYVYVWLSQGLGFRDAIV 60
Db 18 VILVLDVGNNTNIVLGIYNDTKLTAEWRLSTDVLRSADEYGIQVMNLFQQDKLPTLVEGV 77
QY 61 IISSVVPQSIFNLRNLSRRYFNVEPLVIGENAKLGIDVRIEKPSEAGADRLVNAIGAAMV 120
Db 78 IISSVVPNIMYSLEHMIRKRYFKINPLVVGPGIKTGINIKYDNPKEVGADRIVNAVAHEI 137
QY 121 YPGPLVVIDSGTATTFDIVAADGAFEGGIIAPGINLSMQALHEAAKLPRIAIQRPAGNR 180
Db 138 YKRSLLIIDFGTATTFCAVRENGDYLGAICPGIKYSSEALFEKAAKLPVELIKPA--Y 195
QY 181 IVGTDTVSAMQSGVFWGYISLIEGLVARIK-----AERGEPTMTVIATGGVASL 228
Db 196 AICKNTISSIQSGIVRYRLRQVKYLFKELKENLPDGRTRTSLVLTATGGLAKL 248
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RESULT 15

```
AAU91155
ID AAU91155 standard; Protein; 262 AA.
XX
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 24, 2003, 21:27:26 ; Search time 27.207 Seconds
(without alignments)
1297.879 Million cell updates/sec

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Perfect score: 1343
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
tal number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1343	100.0	265	AAU91151	Streptomyces coeli
2	698.5	52.0	272	AAU91152	Mycobacterium tube
3	694.5	51.7	272	AAG81225	Mycobacterium tube
4	663	49.4	258	AAU91172	Pantothenate kinas
5	662	49.3	254	AAU91171	Pantothenate kinas
6	655	48.8	258	AAU01243	B. subtilis novel
7	655	48.8	258	AAU91149	Bacillus subtilis
8	643.5	47.9	256	AAU91175	Pantothenate kinas
9	638	47.5	262	AAU91170	Pantothenate kinas
10	629	46.8	255	AAU91154	Geobacter sulfurre

11	596	44.4	259	23	ABA47661	Listeria monocytog
12	554.5	41.3	233	23	AAU91163	Pantothenate kinas
13	527	39.2	258	23	AAU91153	Rhodobacter capsul
14	517	38.5	260	23	AAU91173	Pantothenate kinas
15	498.5	37.1	250	23	AAU91150	Clostridium acetob
16	492.5	36.7	219	23	AAU91176	Pantothenate kinas
17	409.5	30.5	262	23	AAU91155	Deinococcus radiop
18	342.5	25.5	246	23	AAU91156	Thermotoga maritim
19	295	22.0	257	23	AAU91174	Pantothenate kinas
20	291.5	21.7	273	23	AAU91157	Treponema pallidum
21	280	20.8	212	23	AAU91177	Pantothenate kinas
22	210	15.6	249	23	AAU91178	Pantothenate kinas
23	205.5	15.3	244	23	AAU91168	Pantothenate kinas
24	184	13.7	241	23	AAU91179	Pantothenate kinas
25	181.5	13.5	262	23	AAU91158	Borrelia burgdorfe
26	180.5	13.4	455	21	AAU74910	Neisseria meningit
27	180.5	13.4	592	20	AAU38616	Neisseria meningit
28	180.5	13.4	592	21	AAU74913	Neisseria meningit
29	180.5	13.4	592	23	AAU91166	Pantothenate kinas
30	179	13.3	455	20	AAU38617	Neisseria gonorrh
31	179	13.3	455	21	AAU74908	Neisseria gonorrh
32	179	13.3	460	23	AAU91167	Pantothenate kinas
33	179	13.3	592	20	AAU38618	Neisseria gonorrh
34	179	13.3	592	21	AAU74911	Neisseria gonorrh
35	177	13.2	592	20	AAU38615	Neisseria meningit
36	177	13.2	592	21	AAU74912	Neisseria meningit
37	177	13.2	592	23	AAU91169	Pantothenate kinas
38	176	13.1	249	23	AAU91182	Pantothenate kinas
39	174	13.0	257	23	AAU91160	Synechocystis pant
40	170.5	12.7	389	21	AAU74909	Neisseria meningit
41	139	10.3	242	23	AAU91180	Pantothenate kinas
42	138.5	10.3	248	23	AAU91164	Pantothenate kinas
43	136	10.1	189	20	AAU38614	Neisseria meningit
44	134	10.0	267	23	AAU91162	Bordella pertussis
45	128.5	9.6	229	23	AAU91159	Aquifex aeolicus p

ALIGNMENTS

RESULT 1
AAU91151
ID AAU91151 standard; Protein; 265 AA.
XX
AC AAU91151;
XX
DT 05-JUN-2002 (first entry)
XX
DE Streptomyces coelicolor pantothenate kinase Coax.
XX
KW Pantothenate kinase; Coax; antibiotic; antimicrobial;
KW pantothenate kinase modulator; coenzyme A; bactericidal compound.
XX
OS Streptomyces coelicolor.
XX
PN WO200216601-A2.
XX
PD 28-FEB-2002.
XX
PF 24-AUG-2001; 2001WO-US26531.
XX
PR 24-AUG-2000; 2000US-227860P.
PR 20-MAR-2001; 2001US-0813453.
XX
PA (OMNI-) OMNIGENE BIOPRODUCTS INC.
XX
PI Yocum RR, Patterson TA;
XX
DR WPI; 2002-269358/31.
XX
PT Identifying potential antibiotic or antimicrobial agent, comprises
PT contacting composition comprising pantothenate kinase (Coax) protein
PT with test compound and identifying inhibitor of the Coax protein -

XX PS Claim 10; Page 69-70; 128pp; English.
XX CC The invention describes assays for identifying a (potential) antibiotic
CC comprising contacting an assay composition comprising a pantothenate
CC kinase (Coax) protein with a test compound, and determining the ability
CC of the test compound to inhibit the activity of the Coax protein, an
CC essential enzyme for the production of coenzyme A. Coax protein is a
CC valuable target for identifying bactericidal compounds. Coax modulating
CC agents can be used in an infectious animal model to determine the
CC efficacy, toxicity, or side effects of treatment with such an agent. This
CC is the amino acid sequence of a pantothenate kinase (Coax) protein
CC described in the invention.

XX SQ Sequence 265 AA;
Query Match 100.0%; Score 1343; DB 23; Length 265;
Best Local Similarity 100.0%; Pred. No. 2.2e-122;
Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 MLLTIDVGNTHTVLGLFDGEDIVEHWRISTDSRRTADELAVLQGLMGHPLLGDG 60
1 MLLTIDVGNTHTVLGLFDGEDIVEHWRISTDSRRTADELAVLQGLMGHPLLGDG 60
QY 61 IDGIAICATVPSVLHELREVTTRYGDPVAVLVEPGVKTGPILTDHPKEVGADRIINAV 120
Db 61 IDGIAICATVPSVLHELREVTTRYGDPVAVLVEPGVKTGPILTDHPKEVGADRIINAV 120
QY 121 AAVELYGGPAIVVDFGTATTFDAVSARGEYIGGVIAPIGIEISVEALGVKGAQLRKIEVAR 180
Db 121 AAVELYGGPAIVVDFGTATTFDAVSARGEYIGGVIAPIGIEISVEALGVKGAQLRKIEVAR 180
QY 181 PRSVIGKNTVEAMQSGIVYGAGQVDGVVNRMARELADDDPDDVTVIATGGLAPMVLGESS 240
Db 181 PRSVIGKNTVEAMQSGIVYGAGQVDGVVNRMARELADDDPDDVTVIATGGLAPMVLGESS 240
QY 241 VIDEHEPWLTLMLGLRLVYERNVSRM 265
Db 241 VIDEHEPWLTLMLGLRLVYERNVSRM 265

RESULT 2
AAU91152
ID AAU91152 standard; Protein; 272 AA.
XX AC AAU91152;
XX 05-JUN-2002 (first entry)
XX Mycobacterium tuberculosis pantothenate kinase Coax.
XX KW Pantothenate kinase; Coax; antibiotic; antimicrobial;
KW pantothenate kinase modulator; coenzyme A; bactericidal compound.
XX OS Mycobacterium tuberculosis.
XX PN WO200216601-A2.
XX PD 28-FEB-2002.
XX PF 24-AUG-2001; 2001WO-US26531.
XX PR 24-AUG-2000; 2000US-227860P.
PR 20-MAR-2001; 2001US-0813453.
XX (OMNI-) OMNIGENE BIOPRODUCTS INC.
XX Yocum RR, Patterson TA;
XX WPI; 2002-269358/31.
XX Identifying potential antibiotic or antimicrobial agent, comprises
PT contacting composition comprising pantothenate kinase (Coax) protein

PT XX with test compound and identifying inhibitor of the Coax protein -
PS Claim 10; Page 70-71; 128pp; English.
XX CC The invention describes assays for identifying a (potential) antibiotic
CC comprising contacting an assay composition comprising a pantothenate
CC kinase (Coax) protein with a test compound, and determining the ability
CC of the test compound to inhibit the activity of the Coax protein, an
CC essential enzyme for the production of coenzyme A. Coax protein is a
CC valuable target for identifying bactericidal compounds. Coax modulating
CC agents can be used in an infectious animal model to determine the
CC efficacy, toxicity, or side effects of treatment with such an agent. This
CC is the amino acid sequence of a pantothenate kinase (Coax) protein
CC described in the invention.

XX SQ Sequence 272 AA;
Query Match 52.0%; Score 698.5; DB 23; Length 272;
Best Local Similarity 51.5%; Pred. No. 1.2e-59;
Matches 138; Conservative 53; Mismatches 64; Indels 13; Gaps 3;
QY 1 MLLTIDVGNTHTVLGLFDG---EDIVEHWRISTDSRRTADELAVLQGLMGHPLLGDG 56
Db 1 MLLAIDVRNTHTVVGLLSGMKEHAKVVQQWRIRTESEVTADELALTIDGLIG-----E 53
QY 57 LGDGIDGIAICATVPSVLHELREVTTRYGDPVAVLVEPGVKTGPILTDHPKEVGADRI 116
Db 54 DSERLTGTAALSTVPSVLHEVRIMLDQYWPSVPHVLIIEPGVRTGIPLLVDNPKVEVGADRI 113
QY 117 INAVAAVELYGGPAIVVDFGTATTFDAVSARGEYIGGVIAPIGIEISVEALGVKGAQLRKI 176
Db 114 VNCLAAAYDRFRKAAIVVDFGSSICVDVVSAGKEFLGGAIPGVQVSSDAAAARSALRRV 173
QY 177 EVARPRSVIGKNTVEAMQSGIVYGAGQVDGVVNRMARELA--DDPDDVTVIATGGLAPM 234
Db 174 ELARPRSVVGKNTVECMQAGAVFGFAGLVGDGLVGRIREDSVGSFVDHDAIVATGHTAPL 233
QY 235 VLGESSVIDEHEPWLTLMLGLRLVYERNV 262
Db 234 LIPELHTVDHYDQHLTLQGLRLVFERNL 261

RESULT 3
AAG81225
ID AAG81225 standard; Protein; 272 AA.
XX AC AAG81225;
XX 04-SEP-2001 (first entry)
XX Mycobacterium tuberculosis potential drug target protein SEQ ID 276.
XX KW Drug target; growth; organism viability; characterisation.
XX OS Mycobacterium tuberculosis.
XX PN WO200135317-A1.
XX PD 17-MAY-2001.
XX PF 13-NOV-2000; 2000WO-US31152.
XX PR 12-NOV-1999; 99US-0165086.
PR 12-NOV-1999; 99US-0165124.
PR 01-FEB-2000; 2000US-0179531.
XX (REGC) UNIV CALIFORNIA.
XX Eisenberg D, Rotstein SH, Marcotte EM;
XX WPI; 2001-329193/34.
XX N-PSDB; AAH52076.

PN WO200216601-A2.
XX
PD 28-FEB-2002.
XX
PF 24-AUG-2001; 2001WO-US26531.
XX
PR 24-AUG-2000; 2000US-227860P.
PR 20-MAR-2001; 2001US-0813453.
XX
PA (OMNI-) OMNIGENE BIOPRODUCTS INC.
XX
PI Yocum RR, Patterson TA;
XX
DR WPI; 2002-269358/31.
DR N-PSDB; ABK54168.
XX
PT Identifying potential antibiotic or antimicrobial agent, comprises
PT contacting composition comprising pantothenate kinase (Coax) protein
PT with test compound and identifying inhibitor of the Coax protein -
XX
Claim 10; Page 67-68; 128pp; English.
XX
CC The invention describes assays for identifying a (potential) antibiotic
CC comprising contacting an assay composition comprising a pantothenate
CC kinase (Coax) protein with a test compound, and determining the ability
CC of the test compound to inhibit the activity of the Coax protein, an
CC essential enzyme for the production of coenzyme A. Coax protein is a
CC valuable target for identifying bactericidal compounds. Coax modulating
CC agents can be used in an infectious animal model to determine the
CC efficacy, toxicity, or side effects of treatment with such an agent. This
CC is the amino acid sequence of a pantothenate kinase (Coax) protein
CC described in the invention.
XX
SQ Sequence 258 AA;
Query Match 48.8%; Score 655; DB 23; Length 258;
Best Local Similarity 51.0%; Pred. No. 1.9e-55;
Matches 133; Conservative 46; Mismatches 74; Indels 8; Gaps 3;
QY 1 MLLTIDVGNTHTVLGLFDGEDIVEHWRISTDSRRRTADELAVLLQGLMGHPLLGDELGDG 60
Db 1 LLLVIDVGNTHTVLGVYHDGKLEYHWRIETSRHKTEDEFGMILRSLFDHSGLMFEQ--- 56
QY 61 IDGIAICATVPSVLHELREVTTRYGDVPAVLVEPGVKTGPILTDHPKEVGADRIINAV 120
Db 57 IDGIISSVPPIMFALERMCTKYFHIEPQI-VGPGMKTGLNICYDNPKQVADRIINAV 115
QY 121 AAVELYGGPAIVVDFGTATTFFDAVSARGEYIGGVIAPGIEISVEALGVKGAQLRKIEVAR 180
Db 116 AAHLVGNPLVVDFTATTTCYIDENKQYMGGAIPGTTISTEALYSRAAKLPRIETR 175
QY 181 PRSVIGKNTVEAMQSGIVYGFAGQVDGVVNRMARELADDDVTVIATGGLAPMVLGESS 240
Db 176 PDNIIGKNTVSAMQSGILFGYGVQVEGIVKRMKWA---KQDLKVIATGGLAPLIANESD 232
QY 241 VIDEHEPWLTLMLGLRLVYERN 261
Db 233 CIDIVDPFLTLKGLLEIYERN 253
RESULT 8
AAU91175
ID AAU91175 standard; Protein; 256 AA.
XX
AC AAU91175;
XX
DT 05-JUN-2002 (first entry)
XX
DE Pantothenate kinase (Coax) #13.
DE
KW Pantothenate kinase; Coax; antibiotic; antimicrobial;
KW pantothenate kinase modulator; coenzyme A; bactericidal compound.
XX

Clostridium difficile.
XX
PN WO200216601-A2.
XX
PD 28-FEB-2002.
XX
PF 24-AUG-2001; 2001WO-US26531.
XX
PR 24-AUG-2000; 2000US-227860P.
PR 20-MAR-2001; 2001US-0813453.
XX
PA (OMNI-) OMNIGENE BIOPRODUCTS INC.
XX
PI Yocum RR, Patterson TA;
XX
DR WPI; 2002-269358/31.
DR N-PSDB; ABK54196.
XX
PT Identifying potential antibiotic or antimicrobial agent, comprises
PT contacting composition comprising pantothenate kinase (Coax) protein
PT with test compound and identifying inhibitor of the Coax protein -
XX
Claim 6; Page 105; 128pp; English.
XX
CC The invention describes assays for identifying a (potential) antibiotic
CC comprising contacting an assay composition comprising a pantothenate
CC kinase (Coax) protein with a test compound, and determining the ability
CC of the test compound to inhibit the activity of the Coax protein, an
CC essential enzyme for the production of coenzyme A. Coax protein is a
CC valuable target for identifying bactericidal compounds. Coax modulating
CC agents can be used in an infectious animal model to determine the
CC efficacy, toxicity, or side effects of treatment with such an agent. This
CC is the amino acid sequence of a pantothenate kinase (Coax) protein
CC described in the invention.
XX
SQ Sequence 256 AA;
Query Match 47.9%; Score 643.5; DB 23; Length 256;
Best Local Similarity 49.8%; Pred. No. 2.4e-54;
Matches 130; Conservative 53; Mismatches 71; Indels 7; Gaps 4;
QY 1 MLLTIDVGNTHTVLGLFDGEDIVEHWRISTDSRRRTADELAVLLQGLMGHPLLGDELGDG 60
Db 1 MLLVFDVGNTHTVLGVYKGLVNYWRKTDRKTSDEYGLISNLFYDQV---NISD- 56
QY 61 IDGIAICATVPSVLHELREVTTRYGDVPAVLVEPGVKTGPILTDHPKEVGADRIINAV 120
Db 57 IDDVIISSVVPNMHSLNFENFCIKYCKKQP-LIVGPGIKTGLNICYDNPKQVADRIINAV 115
QY 121 AAVELYGGPAIVVDFGTATTFFDAVSARGEYIGGVIAPGIEISVEALGVKGAQLRKIEVAR 180
Db 116 AGIEKYGAPSVLVDFTATTFFCAISEKGEYLGTTIAPGKISSSEALFQSKLPRVELAK 175
QY 181 PRSVIGKNTVEAMQSGIVYGFAGQVDGVVNRMARELADDDVTVIATGGLAPMVLGESS 240
Db 176 PGMICKSTVSAMQSGIIVGVYGLVDKIISIMKKEL--NCDDVKVIATGGLAKLIASETK 233
QY 241 VIDEHEPWLTLMLGLRLVYERN 261
Db 234 SIDYVDGFLTLGLEGLRIIYEKN 254
RESULT 9
AAU91170
ID AAU91170 standard; Protein; 262 AA.
XX
AC AAU91170;
XX
DT 05-JUN-2002 (first entry)
XX
DE Pantothenate kinase (Coax) #8.
XX
KW Pantothenate kinase; Coax; antibiotic; antimicrobial;

Db 175 RPAGNRIVGTDVTSAMQSGVFWGYISLIEGLV---ARIKAERGEPMTVIATGGVASLFEG 231
QY 238 ESSVIDEHPEPWLTLMLGLRLVYERN 261
Db 232 ATDSIDHFDSDLTIRGLLEIYRRN 255

RESULT 15
AAU91150
ID AAU91150 standard; Protein; 250 AA.
XX
AC AAU91150;
XX
DT 05-JUN-2002 (first entry)
XX
DE Clostridium acetobutylicum pantothenate kinase Coax.
XX
DE
XX
KW Pantothenate kinase; Coax; antibiotic; antimicrobial;
v pantothenate kinase modulator; coenzyme A; bactericidal compound.

-S Clostridium acetobutylicum.
XX
PN WO200216601-A2.
XX
PD 28-FEB-2002.
XX
PF 24-AUG-2001; 2001WO-US26531.
XX
PR 24-AUG-2000; 2000US-227860P.
PR 20-MAR-2001; 2001US-0813453.
XX
PA (OMNI-) OMNIGENE BIOPRODUCTS INC.
XX
PI Yocum RR, Patterson TA;
XX
DR WPI; 2002-269358/31.

XX Identifying potential antibiotic or antimicrobial agent, comprises
PT contacting composition comprising pantothenate kinase (Coax) protein
PT with test compound and identifying inhibitor of the Coax protein -
XX
PS Claim 10; Page 68-69; 128pp; English.
XX
CC The invention describes assays for identifying a (potential) antibiotic
CC comprising contacting an assay composition comprising a pantothenate
CC kinase (Coax) protein with a test compound, and determining the ability
CC of the test compound to inhibit the activity of the Coax protein, an
CC essential enzyme for the production of coenzyme A. Coax protein is a
CC valuable target for identifying bactericidal compounds. Coax modulating
CC agents can be used in an infectious animal model to determine the
CC efficacy, toxicity, or side effects of treatment with such an agent. This
CC is the amino acid sequence of a pantothenate kinase (Coax) protein
CC described in the invention.
SQ Sequence 250 AA;

Query Match 37.1%; Score 498.5; DB 23; Length 250;
Best Local Similarity 43.3%; Pred. No. 3e-40;
Matches 104; Conservative 50; Mismatches 73; Indels 13; Gaps 4;
QY 1 MLLTIDVGNTHFVLGLFDGEDIVEHWRISTDSRTADELAVLLQGLM---GMHPLLGLDEL 57
Db 18 VILVLDVGNTNIVLGIYNDTKLTAEWRLSTDVLRSADEYGIQVMNLFQQDKLDPTL---- 73
QY 58 GDGIDGIAICATVPVSVLHELREVTTRYGDPVAVLVEPGVKTGVPILTDHPKVEGADRII 117
Db 74 ---VEGVIISSVVPNIMYSLEHMIRKYFKINPLV-VGPGIKTGINIKYDNPKEVGADRIV 129
QY 118 NAVAARELYGGPAIVVDFGTATTFDVARSARGEYIGGVIAPIGIEISVEALGVKAQLRKIE 177
Db 130 NAVAAREIYKRSIIIDFGTATTFCVAVRENGDYLGAICPGIKVSSEALFEKAACLPRVE 189

QY 178 VARPRSVIGKNTVEAMQSGIVYGFAGQVDGVVNRMARELADDDPDDVT--VIATGGLAPMV 235
Db 190 LIKPAYAICKNTISSIQSGIVYRYLRQVKYLFKELKENLPDGRRTRTSLVATGGLAKLI 249

Search completed: June 24, 2003, 21:46:12
Job time : 28.207 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 24, 2003, 21:36:04 ; Search time 9.66565 Seconds
(without alignments)
2635.685 Million cell updates/sec

Title: US-09-813-453A-4
Perfect score: 1343
Sequence: 1 MLLTIDVGNTHTVLGLFDGE.....EPWLTLMGLRLVYERNVSRM 265

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1343	100.0	265	2 T36391	hypothetical prote
2	710.5	52.9	274	2 H86937	conserved hypothet
3	698.5	52.0	272	2 A70955	hypothetical prote
4	662	49.3	254	2 F83660	hypothetical prote
5	596	44.4	259	2 AF1102	conserved hypothet
6	596	44.4	273	2 E97293	probable transcrip
7	591	44.0	259	2 AF1464	conserved hypothet
8	554.5	41.3	233	2 S66100	conserved hypothet
9	517	38.5	261	2 B87489	transcription acti
10	409.5	30.5	262	2 E75516	conserved hypothet
11	342.5	25.5	246	2 D72320	conserved hypothet
12	291.5	21.7	273	2 D71326	conserved hypothet
13	181.5	13.5	262	2 F70165	conserved hypothet
14	180.5	13.4	592	2 H82031	probable biotin-la
15	177	13.2	592	2 B81009	BirA protein/Bvg a
16	174	13.0	257	2 S75559	hypothetical prote
17	167	12.4	276	2 A12292	hypothetical prote
18	139	10.3	242	2 A82637	conserved hypothet
19	138.5	10.3	248	2 H83111	hypothetical prote
20	134	10.0	267	2 I40327	baf protein - Bord
21	128.5	9.6	229	2 E70465	hypothetical prote
22	107.5	8.0	465	2 D83598	probable zinc prot
23	107	8.0	198	2 D95285	conserved hypothet
24	107	8.0	383	2 D86781	L-lactate oxidase
25	105.5	7.9	559	2 B75477	conserved hypothet
26	102.5	7.6	336	2 E72359	rod shape-determin
27	102.5	7.6	1036	2 JC5568	serine proteinase
28	102	7.6	781	2 T28750	hypothetical prote
29	101.5	7.6	293	2 AD0913	ribosomal protein

30	101.5	7.6	368	2 B83844	riboflavin specifi
31	101	7.5	420	2 C72774	probable cleavage
32	100	7.4	409	2 JC1378	aryldialkylphospha
33	100	7.4	1763	2 T17465	rifamycin polyketi
34	99.5	7.4	461	2 JE0030	nitrogenase (EC 1.
35	99.5	7.4	575	2 H72752	probable dihydroxy
36	99.5	7.4	705	2 T35165	probable integral
37	98.5	7.3	435	2 F98302	edTA monooxygenase
38	98.5	7.3	435	2 A12980	nitritotriacetate
39	97.5	7.3	367	2 T17481	prephenate dehydro
40	97	7.2	419	2 D84372	pyruvate dehydroge
41	97	7.2	799	2 PC4106	chitinase (EC 3.2.
42	97	7.2	820	2 A40633	chitinase (EC 3.2.
43	97	7.2	990	2 S42586	transposase - Rhiz
44	96.5	7.2	928	2 AF3516	Mg(2+) transport A
45	96	7.1	218	2 S71260	embryonic protein

ALIGNMENTS

RESULT 1

T36391
hypothetical protein SCE94.31c - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jun-2000
C:Accession: T36391
R:Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.
submitted to the EMBL Data Library, April 1999
A:Reference number: Z21573
A:Accession: T36391
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-265 <OLI>
A:Cross-references: EMBL:AL049628; PIDN:CAB40880.1; GSPDB:GN00070; SCOEDB:SCE94.31c
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SCE94.31c
C:Superfamily: Streptomyces coelicolor hypothetical protein SCE94.31c

Query Match 100.0%; Score 1343; DB 2; Length 265;
Best Local Similarity 100.0%; Pred. No. 4.6e-92;
Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MLLTIDVGNTHTVLGLFDGEDIVEHWRISTDSRRTADELAVLLQGLMGHPLLGLDGDG	60
Db	1	MLLTIDVGNTHTVLGLFDGEDIVEHWRISTDSRRTADELAVLLQGLMGHPLLGLDGDG	60
QY	61	IDGIAICATVPSVLHELREVTTRYRGDVPVAVLVEPGVKTGVPILTDPHPKEVGADRIINAV	120
Db	61	IDGIAICATVPSVLHELREVTTRYRGDVPVAVLVEPGVKTGVPILTDPHPKEVGADRIINAV	120
QY	121	AAVELYGGPAIVVDFGTATTFDAVSARGEYIGGVIAPIAGIEISVEALGVKGAQLRKIEVAR	180
Db	121	AAVELYGGPAIVVDFGTATTFDAVSARGEYIGGVIAPIAGIEISVEALGVKGAQLRKIEVAR	180
QY	181	PRSVIGKNTVEAMQSGIVYGAGQVDGVVNRNARELADDDVTVIATGGLAPMVLGESS	240
Db	181	PRSVIGKNTVEAMQSGIVYGAGQVDGVVNRNARELADDDVTVIATGGLAPMVLGESS	240
QY	241	VIDEHEPWLTLMGLRLVYERNVSRM	265
Db	241	VIDEHEPWLTLMGLRLVYERNVSRM	265

RESULT 2

H86937
conserved hypothetical protein ML0232 [imported] - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C:Accession: H86937
R: Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Hol

R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yoshikawa, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, K.; Yata, K.; Yoshida, K
A;Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: E69740
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-233 <KUN>
Cross-references: GB:Z99104; GB:AL009126; NID:g2632267; PIDN:CAB11846.1; PID:el182003;
Experimental source: strain 168
C;Genetics:
A;Start codon: TTG
C;Superfamily: Streptomyces coelicolor hypothetical protein SCE94.31c

Query Match 41.3%; Score 554.5; DB 2; Length 233;
Best Local Similarity 50.5%; Pred. No. 7e-34;
Matches 111; Conservative 39; Mismatches 65; Indels 5; Gaps 2;
QY 1 MLLTIDVGNTHVTLGLFDGEDIVEHWRISTDSRRTADELAVLLQGLMGHPLLDGELG 60
Db 1 MLLVIDVGNTHVTLGVYHDGKLEYHWRISTDSRRTADELAVLLQGLMGHPLLDGELG 56
QY 61 IDGIAICATVPSVLHELREVTTRYGDPVAVLVEPGVKTGPILTDHPKEVGADRIINAV 120
Db 57 IDGIISSVPPIMFALERMCTKYFHIEPQI-VGPGMKTGNIKYDNPKEVGADRIINAV 115
QY 121 AAVELYGGPAIVDFGTATTFDAVSARGEYIGGVIAPIGIEISVEALGVKGAQLRKIEVAR 180
Db 116 AAHLVGNPLIVDFGTATTCYIDENKQYMGGAIAPIGITISTEALYSRAAKLPRIETR 175
QY 181 PRSVIGKNTVEAMQSGIVGFAGQVDGVVNRMARLADDP 220
Db 176 PDNIIGKNTVSAMQSGILFVGQVEGIVKRMKWAQKQDP 215

SULT 9
7489
transcription activator, probable Baf family [imported] - *Caulobacter crescentus*
C;Species: *Caulobacter crescentus*
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: B87489
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of *Caulobacter crescentus*.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: B87489
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-261 <STO>
A;Cross-references: GB:AE005673; NID:g13423392; PIDN:AAK23910.1; GSPDB:GN00148
C;Genetics:
A;Gene: CC1935
C;Superfamily: Streptomyces coelicolor hypothetical protein SCE94.31c

Query Match 38.5%; Score 517; DB 2; Length 261;
Best Local Similarity 42.4%; Pred. No. 4.7e-31;
Matches 112; Conservative 50; Mismatches 90; Indels 12; Gaps 5;

QY 1 MLLTIDVGNTHVTLGLFDGEDIVEHWRISTDSRRTADELAVLLQGLMGHPLLDGELG-D 59
Db 2 MLLAIEQGNNTMFAIHDGASWVAQWRSATSTETFADEYVWLSQLLSM-----QGLGFR 56
QY 60 GIDGIAICATVPSVLHELREVTTRYGDPVAVLVEPGVKTGPILTDHPKEVGADRIINA 119
Db 57 AIDAVIISSVPPQSFNLRNLSRRYFNVEPLVIGE-NAKLIGIDVRIEKPSEAGADRLVNA 115
QY 120 VAAVELYGGPAIVDFGTATTFDAVSARGEYIGGVIAPIGIEISVEALGVKGAQLRKIEVA 179
Db 116 IGAAMVYPGPLVVIDSGTATTFDIVAADGAFEGGIAPGINLSMQALHEAAAKLPRIATQ 175
QY 180 RP--RSVIGKNTVEAMQSGIVGFAGQVDGVVNRMARLADDPDDVTVIATGGLAPMVLG 237
Db 176 RPAGNRIVGTDTVSAMQSGVFWGYISLIEGLV--ARIKAERGEPMVTVIATGGVASLFEG 232
QY 238 ESSVIDEHPEPWLTLMLGLRLVYERN 261
Db 233 ATDSIDHFDSDLTIRGLLEIYRRN 256

RESULT 10
E75516
conserved hypothetical protein - *Deinococcus radiodurans* (strain R1)
C;Species: *Deinococcus radiodurans*
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 20-Jun-2000
C;Accession: E75516
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: E75516
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-262 <WHI>
A;Cross-references: GB:AE001905; GB:AE000513; NID:g6458144; PIDN:AAF10040.1; PID:g64;
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR0461
A;Map position: 1
C;Superfamily: Streptomyces coelicolor hypothetical protein SCE94.31c

Query Match 30.5%; Score 409.5; DB 2; Length 262;
Best Local Similarity 37.9%; Pred. No. 4.1e-23;
Matches 97; Conservative 44; Mismatches 102; Indels 13; Gaps 4;

QY 2 LLTIDVGNTHVTLGLFDGEDIVEH-WRISTDSRRTADELAVLLQGLMGHPLLDGELG 60
Db 6 LLAVDIGNTTVTLGLADASGALTHTWRIRTNREMLPDDLALQLHGLFTL-----AGAP 58
QY 61 IDGIAICATVPSVLHELREVTTRYGDPVAVLVEPGVKTGPILTDHPKEVGADRIINAV 120
Db 59 IPRAAVLSSVAPPVGENYALAKRHFMDAFSAENLPDVTVELDTPGSGVAGADRLCNLF 118
QY 121 AAVELYGG--PAIVDFGTATTFDAVSARGEYIGGVIAPIGIEISVEALGVKGAQLRKIEV 178
Db 119 GAELYGLLDYAVVDFGTSTNFDVVGRGRFLGGILATGAQVSADALFARAACLPRITL 178
QY 179 ARPRSVIGKNTVEAMQSGIVGFAGQVDGVVNRMARLADDPDDVTVIATGGLAPMVLGE 238
Db 179 QAPETAIGKNTVHALQSLVFGYAEVMVDGLLRIRRAEL---PGEAVAVATGGSRTVQGI 235
QY 239 SSVIDEHPEPWLTLMLGL 254
Db 236 CQEIDYDETLTLRGL 251

RESULT 11
D72320
conserved hypothetical protein - *Thermotoga maritima* (strain MSB8).
C;Species: *Thermotoga maritima*

A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: H82031
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-592 <PAR>
A;Cross-references: GB:AL162752; GB:AL157959; NID:g7378778; PIDN:CAB83659.1; PID:g737911
A;Experimental source: serogroup A, strain 22491
C;Genetics:
A;Gene: birA; NMA0357
C;Keywords: ligase

Query Match 13.4%; Score 180.5; DB 2; Length 592;
Best Local Similarity 27.0%; Pred. No. 9.1e-06;
Matches 67; Conservative 35; Mismatches 103; Indels 43; Gaps 8;
QY 28 ISTDSRRRTADELAVLLQG-----LMGMHPL-----LGDELGDGID----- 62
Db 329 VSVPKRRDSEFLLLDGGNSRLKWAWVENGTFATVGSAPYRDLSPGAEWAEEKVDGNVRI 388
63 -GIAICATVPSVLHELREVTTRYGDPVPAVLVEPGVKTPILTDHPKEVGADRIINAVA 121
Db 389 VGCAVCGEFKKA--QVQELARKIEWLPSSAQALGIRNHY----RHPEEHGSDRFWNLG 442
QY 122 AVELYGGPAIVVDFGTATTFDAVSARGEYIGGVIAPGIEISVEALGVKGAQLRKIEVARP 181
Db 443 SRRFSRNACVVVSCGTAVTDALTDGHHYLGTTIMPGFHLMKESLAVRTANLNR--HAGK 500
QY 182 RSVIGKNTVEAMQSGIVYGFAGQVDGVVNRMARLADDDVTVIATGG-----LAP 233
Db 501 RYPPPTTTGNAVASGMDAVCGSVMMMHGRL-KEKTGAGKPDVDVIITGGAAKVAEALPP 559
QY 234 MVLGESSV 241
Db 560 AFLAENTV 567

RESULT 15
B81009

BirA protein/Bvg accessory factor NMB2075 [imported] - Neisseria meningitidis (strain MC58)
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: B81009
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Vignani, R.; Tettelin, H.; et al.
Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
Reference number: A81000; MUID:20175755; PMID:10710307
Accession: B81009
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-592 <TET>
A;Cross-references: GB:AE002557; GB:AE002098; NID:g7227332; PIDN:AAF42394.1; PID:g722733
A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB2075

Query Match 13.2%; Score 177; DB 2; Length 592;
Best Local Similarity 30.5%; Pred. No. 1.7e-05;
Matches 60; Conservative 28; Mismatches 89; Indels 20; Gaps 6;

QY 56 ELGDG--IDGIAICATVPSVLHELREVTTRYGDPVPAVLVEPGVKTPILTDHPKEVG 112
Db 380 EKADGNVRIVGCAVCGEFKKA--QVQELARKIEWLPSSAQALGIRNHY----RHPEEHG 433
QY 113 ADRIINAVAARELYGGPAIVVDFGTATTFDAVSARGEYIGGVIAPGIEISVEALGVKGAQ 172
Db 434 SDRWFNALGSRFRSRNACVVVSCGTAVTDALTDGHHYLGTTIMPGFHLMKESLAVRTAN 493
QY 173 LRKIEVARPRSVIGKNTVEAMQSGIVYGFAGQVDGVVNRMARLADDDVTVIATGG-- 230
Db 494 LNR--HAGKRYPPPTTTGNAVASGMDAVCGSVMMMHGRL-KEKTGAGKPDVDVIITGGGA 550

QY 231 -----LAPMVLGESSV 241
Db 551 AKVAEALPPAFLAENTV 567

Search completed: June 24, 2003, 22:02:59
Job time : 11.6657 secs

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OM protein - protein search, using sw model

Run on: June 24, 2003, 21:33:11 ; Search time 4.60909 Seconds
(without alignments)
2384.688 Million cell updates/sec

Title: US-09-813-453A-4
Perfect score: 1343
Sequence: 1 MLLTIDVGNTHTVLGLFDGE.....EPWLTLMGLRLVYERNVSRM 265

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	554.5	41.3	233	1	YACB_BACSU	P37564 bacillus su
2	134	10.0	267	1	BAF_BORPE	Q45338 bordetella
3	99.5	7.4	461	1	NIFN_RHOCA	P19077 rhodobacter
4	99.5	7.4	557	1	ILVD_AERPE	Q9Yg88 aeropyrum p
5	99.5	7.4	705	1	MMLC_STRCO	O88022 streptomyce
6	97.5	7.3	472	1	KPYK_MYCIT	P94939 mycobacteri
7	97	7.2	820	1	CHIA_ALTSO	P32823 alteromonas
8	96.5	7.2	811	1	MUTS_THEAQ	Q56215 thermus aqu
9	95.5	7.1	438	1	TUD4_AGRVI	Q44472 agrobacteri
10	95.5	7.1	472	1	KPYK_MYCTU	O06134 mycobacteri
11	95	7.1	279	1	TRPA_RHILO	Q98cn6 rhizobium l
12	95	7.1	321	1	GLK_BACSU	P54495 bacillus su
13	93.5	7.0	242	1	HIS4_HALN1	Q9hnl4 halobacteri
14	93.5	7.0	293	1	PRMA_ECOLI	P28637 escherichia
15	93	6.9	355	1	BUK1_CLOAB	Q45829 clostridium
16	93	6.9	639	1	YGFT_ECOLI	Q46820 escherichia
17	93	6.9	697	1	YN26_MYCTU	P71886 mycobacteri
18	92.5	6.9	525	1	GUAA_PSEAE	Q9hxm6 pseudomonas
19	92	6.9	261	1	PYRH_MYCTU	Q10791 mycobacteri
20	91.5	6.8	1113	1	CARB_CORGL	P58939 corynebacte
21	91	6.8	1101	1	GUNC_CELFI	P14090 cellulomona
22	90.5	6.7	973	1	UVRA_RHIME	P56899 rhizobium m
23	90	6.7	284	1	LPXD_METCA	Q9aip8 methylococc
24	90	6.7	397	1	TYRB_SALTY	P74861 salmonella
25	90	6.7	397	1	SYL_METHH	O27552 methanobact
26	89.5	6.7	269	1	TRCI_STRCO	O68814 streptomyce
27	89.5	6.7	553	1	SYE_METHH	O26157 methanobact
28	89.5	6.7	708	1	TRP_NEUCR	P13228 neurospora
29	88.5	6.6	277	1	PANB_BACSU	P52996 bacillus su
30	88.5	6.6	449	1	TRB2_AERPE	Q9Y9h2 aeropyrum p
31	88	6.6	379	1	AMPC_MORMO	P94958 morganella
32	87	6.5	517	1	MURF_MYCLE	O69556 mycobacteri
33	87	6.5	821	1	CLPC_PORPU	P51332 porphyra pu

34	86.5	6.4	335	1	GPDA_ARCFU	O29390 archaeoglob
35	86.5	6.4	429	1	YN05_MYCTU	Q50660 mycobacteri
36	86	6.4	269	1	THIG_CAUCR	Q9a746 caulobacter
37	86	6.4	327	1	PXA2_SALFI	P58716 salmonella
38	85.5	6.4	265	1	Y309_HALN1	Q9hsb8 halobacteri
39	85.5	6.4	304	1	PHEA_AMEME	Q44104 amycolatops
40	85.5	6.4	349	1	RUVB_MYCLE	P40833 mycobacteri
41	85.5	6.4	475	1	KPYK_CORGL	Q46078 corynebacte
42	85.5	6.4	1018	1	HMW1_MYCPN	Q50365 mycoplasma
43	85	6.3	327	1	PXA2_SALTY	P58718 salmonella
44	85	6.3	379	1	FTSZ_MYCTU	O08378 mycobacteri
45	85	6.3	427	1	SYH_MYCLE	P46696 mycobacteri

ALIGNMENTS

RESULT 1
YACB_BACSU
ID YACB_BACSU STANDARD; PRT; 233 AA.
AC P37564;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein yacB.
GN YACB.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=96051385; PubMed=7584024;
RA Ogasawara N., Nakai S., Yoshikawa H.;
RT "Systematic sequencing of the 180 kilobase region of the Bacillus
subtilis chromosome containing the replication origin.";
RL DNA Res. 1:1-14(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Danzot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
Parro V., Pohl T.M., Portetelle D., Porvollik S., Prescott A.M.,
Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Sekiguchi J., Sekowska A., Seror S.J., Serro P., Shin B.S., Soldo B.,
Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
subtilis.";
RL Nature 390:249-256(1997).

-I- SIMILARITY: SOME, TO B.PERTUSSIS BVG ACCESSORY FACTOR.


```

OC Altermonas.
OX NCBI_TaxID=29458;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93106952; PubMed=8416892;
RA Tsujibo H., Orikoshi H., Tanno H., Fujimoto K., Miyamoto K.,
RA Imada C., Okami Y., Inamori Y.;
RT "Cloning, sequence, and expression of a chitinase gene from a marine
RL bacterium, Altermonas sp. strain O-7.";
RN J. Bacteriol. 175:176-181(1993).
RP [2]
RX SEQUENCE OF 22-48, AND CHARACTERIZATION.
RA MEDLINE=93099552; PubMed=1464065;
RA Tsujibo H., Yoshida Y., Miyamoto K., Imada C., Okami Y., Inamori Y.;
RT "Purification, properties, and partial amino acid sequence of
RL chitinase from a marine Altermonas sp. strain O-7.";
RN Can. J. Microbiol. 38:891-897(1992).
RP [3]
RX MUTAGENESIS.
RA MEDLINE=93379363; PubMed=7764022;
RA Tsujibo H., Orikoshi H., Imada C., Okami Y., Miyamoto K.,
RL Inamori Y.;
RT "Site-directed mutagenesis of chitinase from Altermonas sp. strain
RL O-7.";
RL Biosci. Biotechnol. Biochem. 57:1396-1397(1993).
CC -|- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-
CC acetyl-D-glucosamine polymers of chitin.
CC -|- ENZYME REGULATION: Stimulated by magnesium ions; inhibited by
CC N-bromosuccinimide and 2-hydroxy-5-nitrobenzyl bromide.
CC -|- MISCELLANEOUS: THE OPTIMUM PH AND TEMPERATURE OF CHI-A ARE 8.0 AND
CC 50 DEGREES CELSIUS, RESPECTIVELY.
CC -|- SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF GLYCOSYL
CC HYDROLASES).
CC -----
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CC -----
DR EMBL; AB063629; BAB79620.1; -.
DR HSSP; P07254; ICTN.
DR InterPro; IPR003610; CBM_5_12.
DR InterPro; IPR001579; Chitinase_18/2.
DR InterPro; IPR001223; Glyco_hydro_18.
DR InterPro; IPR000601; PKD_domain.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR Pfam; PF00801; PKD; 2.
DR Pfam; PF02839; CBM_5_12; 1.
DR ProDom; PD000471; Glyco_hydro_18; 1.
DR SMART; SM00112; CA; 1.
DR SMART; SM00495; ChtBD3; 1.
DR SMART; SM00089; PKD; 2.
DR PROSITE; PS01095; CHITINASE_18; 1.
KW Hydrolase; Glycosidase; Chitin degradation; Signal.
FT SIGNAL 1 21
FT CHAIN 22 820
FT ACT_SITE 313 313
FT PROTON_DONOR (BY SIMILARITY).
SQ SEQUENCE 820 AA; 87346 MW; FFD70D91192BA320 CRC64;

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QY 102 --PILTDHPKEVGAD-----RIINAVAAVELYG-GPAIVV 133
DQ 408 GSHLSTDECNGTGVDNDGVPKGPAYTGDHAIQLLLQGVQPSKLVMGVAMYGRGWGLV 467
QY 134 DFGTATTFDAVSA-----RGEYIGGVIAPGI-----EISVEALGVKGAQLRKIEVA---- 179
DQ 468 DANAAPGNPWTAPNGNPLTGTSTSEGVWEPGIMDYKATAANAVGGGSGVNGYEVGYDEQ 527
QY 180 -----RPRSVIGK-----NT-----VEAMQSGIVY 199
DQ 528 AQAAYVWNRSGKLITYDSPRSVIAKQYANTHQLAGLFGWEIDADNGDILNAMYDGLTA 587
QY 200 G-----FAGQVDGVVNRMARLADDDVTVIATGGLA 232
DQ 588 GEIPNRAPTIGVSGPINVTSGQVWV-VDAQASDLNDPLTYSWAAPGLA 636

RESULT 8
MUTS_THEAQ
ID MUTS_THEAQ STANDARD; PRT; 811 AA.
AC Q56215;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE DNA mismatch repair protein mutS.
GN MUTS.
OS Thermus aquaticus.
OC Bacteria; Thermus/Delnococcus group; Delnococei; Thermales;
OC Thermaceae; Thermus.
OX NCBI_TaxID=271;
RN {1}
RP SEQUENCE FROM N.A.
RC STRAIN-YT1;
RX MEDLINE=96214934; PubMed=8617781;
RA Biswas I., Hsieh P.;
RT "Identification and characterization of a thermostable MutS homolog
from Thermus aquaticus.";
RL J. Biol. Chem. 271:5040-5048(1996).
CC -!- FUNCTION: This protein is involved in the repair of mismatches in
DNA. It is possible that it carries out the mismatch recognition
step. This protein has a weak ATPase activity.
CC -!- SIMILARITY: BELONGS TO THE DNA MISMATCH REPAIR MUTS FAMILY.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
DQ EMBL: U33117; AAC43637.1; -.
DR InterPro; IPR000432; MutS_C.
DR InterPro; IPR002863; MutS_N.
DR Pfam; PF00488; MutS_C; 1.
DR Pfam; PF01624; MutS_N; 1.
DR ProDom; PD001263; MutS_C; 1.
DR SMART; SM00534; MUTSAC; 1.
DR SMART; SM00533; MUTSD; 1.
DR TIGRFAMs; TIGR01070; mutS1; 1.
DR PROSITE; PS00486; DNA_MISMATCH_REPAIR_2; 1.
KW DNA repair; ATP-binding; DNA-binding.
FT NP_BIND 583 590 ATP (POTENTIAL).
SQ SEQUENCE 811 AA; 90627 MW; 43A5E5296A333515 CRC64;

```

Query Match	7.2%;	Score 96.5;	DB 1;	Length 811;
Best Local Similarity	26.3%;	Pred. No. 8.9;		
Matches 51;	Conservative 28;	Mismatches 58;	Indels 57;	Gaps 9;
QY	37	DELA	VLLQGLMGHPLLGDG	---IDGIAICATVPSVLHELREVT--RRYYGDVPAV 91
		:	! ! ! ! !	: ! ! ! ! !
db	644	EEVA	LILKEATENSVLLDEVGRGTSSLDGVAIATAVAEALHERRAYTLFATHYFELTA-	702

QY 92 LVPEGVKGVPIILTDHPKEVGADRIINA-VAARELYGGPAIVVDFGATTFDAVSARGEY 150
Db 703 -----LGLPRLKNLHVAAREEAGGLVY-----HQV 728
QY 151 IGGVIAPGIEISVEALGVKGAQLRKIEVARPSVIGKNTVEAMQSGIVYGFAGQVDGVVN 210
Db 729 LPGPASKSYGVEVAAM-----AGLPKEVVARARALL-----QAMAA-----RREGALDAVLE 775
QY 211 RMARELADDDPDVDT 224
Db 776 RL---LALDDPDLT 786

RESULT 9
TUD4_AGRVI
ID TUD4_AGRVI STANDARD; PRT; 438 AA.
AC Q44472;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Putative hydroxypyruvate reductase (EC 1.1.1.81).
GN TTUD.
OS Agrobacterium vitis (Rhizobium vitis).
OG Plasmid pTRAB4.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=373;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AB4;
RX MEDLINE=96062236; PubMed=7592429;
RA Crouzet P., Otten L.;
RT "Sequence and mutational analysis of a tartrate utilization operon
from Agrobacterium vitis.";
RL J. Bacteriol. 177:6518-6526(1995).
CC -!- FUNCTION: DEGRADES AN UNIDENTIFIED TOXIC PRODUCT FROM THE FIRST
CC STEP OF TARTRATE DEGRADATION.
CC -!- CATALYTIC ACTIVITY: D-glycerate + NAD(P)(+) -> hydroxypyruvate +
CC NAD(P)H.
CC -!- PATHWAY: Tartrate degradation; second step.
CC -!- INDUCTION: BY TARTRATE.
CC -----
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CC -----
CC EMBL; U25634; AAA68699.1; -.
DR InterPro; IPR005346; UPF0125.
DR Pfam; PF03658; UPF0125; 1.
KW Plasmid; Oxidoreductase; NADP.
SQ SEQUENCE 438 AA; 44730 MW; 38C75BAFFFB0636B CRC64;

Query Match 7.1%; Score 95.5; DB 1; Length 438;
Best Local Similarity 26.1%; Pred. No. 5.4;
Matches 57; Conservative 28; Mismatches 78; Indels 55; Gaps 13;
QY 52 LLGDELGDGIDGIAICATV--PSVLHELREVTTRYGDVP-----AVLVEPGVKGTGPILT 105
Db 202 IISDVPGDPPSEIASGPTVADPTTLADAAAIARYGIDLPSARAVLVQ-GNET----- 254
QY 106 DHPK--EVGADRIINAVAARELYGGPAIVVDFGATTF--DAVSARGEYIGGVIAPGIEI 161
Db 255 --PRAGEVAGEIRLVAAAPSIALAAAAALDAGLCPLILGDALEGEAREMGRVMA-GIAL 311
QY 162 SVEALGVKGAQLRKIEVARPSVI--GKNTVE--AMQSGI----- 197
Db 312 SARDKG-----LPVAAPAVILSGGESTVSLGAMTEGRGGRNTEFFLLSLAVALKGASG 363

QY 198 VYGFAGQVDGV--VNRMARELADDDPDVTVIATGGGLAP 233
Db 364 IWAIAGDTGDGIDGVEDAAGALV-APDSLIRMRDAGIDP 400
RESULT 10
KPYK_MYCTU
ID KPYK_MYCTU STANDARD; PRT; 472 AA.
AC O06134;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pyruvate kinase (EC 2.7.1.40) (PK).
GN PYK OR PYKA OR RV1617 OR MT1653 OR MTCY01B2.09.
OS Mycobacterium tuberculosis
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
laboratory strains.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ATP + pyruvate -> ADP + phosphoenolpyruvate.
CC -!- COFACTOR: REQUIRES MAGNESIUM AND POTASSIUM.
CC -!- PATHWAY: Glycolysis; final step.
CC -!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE PYRUVATE KINASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z95554; CAB08894.1; -.
DR EMBL; AE007029; AAK45923.1; -.
DR HSSP; P14178; 1EOT.
DR TIGR; MT1653; -.
DR TubercuList; RV1617; -.
DR InterPro; IPR001697; Pyruvate_kinase.
DR Pfam; PF00224; PK; 1.
DR Pfam; PF02887; PK_C; 1.
DR PRINTS; PR01050; PYRUVTKNASE.
DR ProDom; PD001009; Pyruvate_kinase; 1.
DR TIGRFAMs; TIGR01064; pyruv_kin; 1.
DR PROSITE; PS00110; PYRUVATE_KINASE; 1.
KW Transferase; Kinase; Glycolysis; Magnesium; Complete proteome.
FT ACT_SITE 218 218 BY SIMILARITY.
FT METAL 220 220 MAGNESIUM (BY SIMILARITY).

FT METAL 241 241 MAGNESIUM (BY SIMILARITY).
FT METAL 242 242 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 472 AA; 50699 MW; 2228960E0A45806B CRC64;

Query Match 7.1%; Score 95.5; DB 1; Length 472;
Best Local Similarity 21.9%; Pred. No. 5.8;
Matches 54; Conservative 39; Mismatches 89; Indels 65; Gaps 11;

QY 5 IDVGNTHTVLGLFDGEDIVEHWRISTDSRRTADELAVLLQGLMGHPLLGLDE----- 56
Db 124 VDDGKVALVDAVEGDDV---CTVVEGGPVSNDKGISLPGMNVTPALSEKDIEDLTFA 180

QY 57 LGDGDIDGIAIC-ATVPSVLHELREVTTRYGGDPAVLVEPGVKTGPILTQHPKEVGADR 115
Db 181 LNLGVDMAVSFVRSPADVELVHEVMDR-----IGRRVPVIAKLEKPEAIDN 227

QY 116 IINAVAAVELYGGPAIVVDGTTATTFDAVS-ARGEYIGGVIAPGIEISVEALGVKGAQLR 174
Db 228 L-----EAIVL-----AFDAMVARGDL-----GVLPLEEVPL--VQKR 260

175 KIEVARPRSVIGKNTVEAMQSGIVYGFAGQVDGVVNRMARLADDDVTVIATGGLAPM 234
Db 261 AIQMARENA---KPVIVATQ-----MLDSMIENSRPTRAESDVANAVLDGADALM 308

QY 235 VLGESSV 241
Db 309 LSGETSV 315

RESULT 11
TRPA_RHILO STANDARD; PRT; 279 AA.
AC Q98CN6;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tryptophan synthase alpha chain (EC 4.2.1.20).
GN TRPA OR MLR5073.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
Mochizuki Y., Nakayama S., Nakazaki N., Shlimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.;
RA "Complete genome structure of the nitrogen-fixing symbiotic bacterium
Mesorhizobium loti.";
RT DNA Res. 7:331-338(2000).
RL -!- FUNCTION: The alpha subunit is responsible for the aldol cleavage
of indoleglycerol phosphate to indole and glyceraldehyde 3-
phosphate.
CC -!- CATALYTIC ACTIVITY: L-serine + 1-(indol-3-yl)glycerol 3-phosphate
- L-tryptophan + glyceraldehyde 3-phosphate + H(2)O.
CC -!- PATHWAY: Tryptophan biosynthesis; fifth (last) step.
CC -!- SUBUNIT: Tetramer of two alpha and two beta chains (By
similarity).
CC -!- SIMILARITY: BELONGS TO THE TRPA FAMILY.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AP003005; BAB51585.1; -

DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR002028; trp_synthaseA.
DR Pfam; PF00290; trp_syntA; 1.
DR ProDom; PD001535; TRP_synthase_alpha; 1.
DR TIGRFAMs; TIGR00262; trpA; 1.
DR PROSITE; PS00167; TRP_SYNTHASE_ALPHA; 1.
KW Tryptophan biosynthesis; Lyase; Complete proteome.
SQ SEQUENCE 279 AA; 29129 MW; 0D83F876B77608FA CRC64;

Query Match 7.1%; Score 95; DB 1; Length 279;
Best Local Similarity 22.7%; Pred. No. 3.6;
Matches 52; Conservative 31; Mismatches 94; Indels 52; Gaps 10;

QY 19 GEDIVEHWRISTDSRRTADELAVLLQG-----LMGMHPLLGLDELGDGIDGIAICATVPS 72
Db 76 GQTLVKTLKMASEFRAGDNETPIVLMGYNPIYIYGVDRLKDALASGIDGLIVVDLPPE 135

QY 73 VLHELREVTTRYGGDPAVLVEPGVKTGPILT---TDHPKEVGADRIINAVAAVELYGGP 129
Db 136 MDEE-----LCIPALKAGINFIRLATPTTDDKRLPKVLQNTSGFVYVSM 180

QY 130 AIVVDFGTATTFDAVSARGEYIGGVIAPGIEISVEALGVKGAQLRKIEVARPRSVIGKNT 189
Db 181 TGITGSALADTGKVAANVRNIKGHTDLP---VCV-GFGVKTA-----EQAR---VIGANA 228

QY 190 VEAMQSGIVYGFAGQVDGVVNRMAR-----ELADDDVTVIATGGLA 232
Db 229 -----DGVVVVGT-----IVNAVANVLGPKGKTKTADPAEAVATLVSGLA 267

RESULT 12
GLK_BACSU STANDARD; PRT; 321 AA.
AC P54495;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Glucokinase (EC 2.7.1.2) (Glucose kinase).
GN GLCK.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / JH642;
RX MEDLINE=97124195; PubMed=8969508;
RA Mizuno M., Masuda S., Takemaru K.-I., Hosono S., Sato T., Takeuchi M.,
Kobayashi Y.;
RT "Systematic sequencing of the 283 kb 210 degrees-232 degrees region of
the Bacillus subtilis genome containing the skin element and many
sporulation genes".
RL Microbiology 142:3103-3111(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
Joris B., Karamata D., Kasahara Y., Klaer-Blanchard M., Klein C.,
Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

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OM protein - protein search, using sw model

Run on: June 24, 2003, 21:35:06 ; Search time 21.6135 Seconds
(without alignments)
2526.317 Million cell updates/sec

Title: US-09-813-453A-4
Perfect score: 1343
Sequence: 1 MLTIDVGNTHTVLGLFDE.....EPWLTMLGLRLVYERNVSRM 265

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
otal number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archheap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1343	100.0	265	16 Q9X8N6	Q9x8n6 streptomyce
2	710.5	52.9	274	16 Q9CD56	Q9cd56 mycobacteri
3	698.5	52.0	272	16 O06282	O06282 mycobacteri
4	667	49.7	258	2 Q9F985	Q9f985 bacillus st
5	662	49.3	254	16 Q9KGH5	Q9kgH5 bacillus ha
6	639	47.6	255	16 Q8R7M2	Q8r7m2 thermoanaer
7	636	47.4	259	16 Q8XHL5	Q8xhl5 clostridium
8	596	44.4	259	16 Q8YAC5	Q8yac5 listeria mo
9	596	44.4	273	16 Q97EB4	Q97eb4 clostridium
10	591	44.0	259	16 Q92F54	Q92f54 listeria in
11	517	38.5	261	16 Q9A621	Q9a621 caulobacter
12	409.5	30.5	262	16 Q9RX54	Q9rx54 deinococcus
13	373	27.8	256	16 Q8RFE4	Q8rfe4 fusobacteri
14	342.5	25.5	246	16 Q9WZY5	Q9wzy5 thermotoga
15	291.5	21.7	273	16 O83446	O83446 treponema p
16	280	20.8	212	2 O32514	O32514 desulfovibr

17	181.5	13.5	262	16	O51477	O51477 borrelia bu
18	180.5	13.4	592	16	Q9JWI7	Q9jwi7 neisseria m
19	177	13.2	592	16	Q9JXF1	Q9jxf1 neisseria m
20	174	13.0	257	16	P74045	P74045 synechocyst
21	167	12.4	276	16	Q8YQD7	Q8yqD7 anabaena sp
22	164	12.2	295	16	Q8Y2M4	Q8y2m4 ralstonia s
23	139	10.3	242	16	Q9PCI4	Q9pci4 xylella fas
24	138.5	10.3	248	16	Q9HWC1	Q9hwc1 pseudomonas
25	128.5	9.6	229	16	O67753	O67753 aquifex aeo
26	112	8.3	56	2	P94305	P94305 bacillus ps
27	107.5	8.0	465	16	Q916C2	Q916c2 pseudomonas
28	107	8.0	198	16	Q930K7	Q930k7 rhizobium m
29	107	8.0	383	16	Q9CG58	Q9cg58 lactococcus
30	105.5	7.9	559	16	Q9RW79	Q9rw79 deinococcus
31	105.5	7.9	1036	2	Q54483	Q54483 serratia ma
32	102.5	7.6	336	16	Q9WZ57	Q9wz57 thermotoga
33	102	7.6	697	5	Q8T8N8	Q8t8n8 caenorhabdi
34	102	7.6	755	5	Q9BIC3	Q9bic3 caenorhabdi
35	102	7.6	781	5	Q9GYT0	Q9gyt0 caenorhabdi
36	101.5	7.6	293	16	Q8XGI2	Q8xgi2 salmonella
37	101.5	7.6	368	16	Q9KCL7	Q9kcl7 bacillus ha
38	101	7.5	420	17	Q9YFR8	Q9yfr8 aeropyrum p
39	100.5	7.5	522	2	Q9Z692	Q9z692 streptococc
40	100	7.4	409	2	Q50432	Q50432 mycobacteri
41	100	7.4	1762	2	O52546	O52546 amycolatops
42	100	7.4	1763	2	O52790	O52790 amycolatops
43	100	7.4	3562	2	Q9F829	Q9f829 micromonosop
44	99	7.4	759	2	O86044	O86044 bordetella
45	99	7.4	1053	16	Q9RK93	Q9rk93 streptomyce

ALIGNMENTS

RESULT 1
Q9X8N6 PRELIMINARY; PRT; 265 AA.
ID Q9X8N6;
AC Q9X8N6;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Hypothetical protein SCO3380.
GN SCO3380 OR SCE94.31C.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Oliver K., Harris D.;
RL Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapaitte D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

QY	60	GIDGIAICATVP	SVLHELREVT	RRYYGDVPAVLVE	-----PGVK-TGVPILTDHP	108
		:	:	:	:	
Db	58	-VDAILISSVVP	NIITFOFARKYF	-KVEATIVDLEKKLP	FTFAKGINVTG-----	107
QY	109	KEVGADRIINA	VAVELYGGPAIVV	-DFGTATTFDAVSARGEY	IGGVIAPGIEISVEALG	167
			:	:	:	:
Db	108	--FGADRIIDI	TEAMQKYPDKNLV	IFDFGTATTYD-VLKKGVY	IGGGILPGIDMSINALY	164
QY	168	VKGAQLRKIEA	RRPSRVICKNTVEAMQ	SGIVYGFAGQVDGVVNR	MARELADDDDDVTVIA	227
		:	:	:	:	:
Db	165	GNTAKLPRVKF	TTTPSSVLGDTMKQIQ	AAIFFGYAGQIKHIIK	INEEL---NEEIFVLA	221
QY	228	TGGLAPMVLG	ESSVIDEHPEWLTLMGL	RVLVYERN	261	
			:	:	:	
Db	222	TGGLGKILSAE	IDEIDEYDANLSLKG	LYTLTKLN	255	

RESULT 14

Q9WZY5 PRELIMINARY; PRT; 246 AA.
Q9WZY5;
01-NOV-1999 (TReMBLrel. 12, Created)
01-NOV-1999 (TReMBLrel. 12, Last sequence update)
01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Hypothetical protein TM0883.
GN TM0883.
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB8 / DSM 3109;
RX MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Raft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima."
RL Nature 399:323-329(1999).
DR EMBL; AE001754; AAD35964.1; -.
DR TIGR; TM0883; -.
DR InterPro; IPR004619; Baf.
DR Pfam; PF03309; Bvg_acc_factor; 1.
DR TIGRFAMs; TIGR00671; baf; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 246 AA; 27154 MW; 9E0309AD462CF266 CRC64;

Query Match	25.5%;	Score 342.5;	DB 16;	Length 246;	
Best Local Similarity	35.7%;	Pred. No. 5.2e-17;			
Matches	92;	Conservative 45;	Mismatches 98;	Indels 23; Gaps 9;	
QY	1	MLLTIDVGNTHTVLGFDCGEDI	VEHWRISTDSRRRTADELAVLLQGLGMHPLLGLDGDG	60	
Db	1	MYLLVDVGNTHSVFSITEDGKTFRRWRLSTGVFQTEDEL-----FSLHLPLGLGDAMRE-	53		
QY	61	IDGIAICATVP	SVLHELREVT	RRYYGDVPA-VLVEPG-VKTGVPILTDHPKEVGADRIIN	118
Db	54	IKGIGVASVPTQNTVIERFSQKYFHISPIWVKAKNGCVKWNV----	KNPSEVGADRVAN	109	
QY	119	AVAAVELYGGPA	IVVDFGTATTFDAVSARGEYIGGVIA	PGIEISVEALGVKGAQLRKIEV	178
Db	110	VVAFVKEYGKNGIIIDMTATTVDLV-VNGSYEGGAILPGFFMMVHSLFRGTAKLPLVEV	168		
QY	179	ARPRSVIGKNTVEAMSGI	VYGFAGQVDGVVNR	MARELADDDVTVIATGGLAPMV--L	236
Db	169	KPADFVVGKDTEENIRLGVVNGSVYALEGII	GRIKEVYGDLP----	VVLTTGGQSKIVKDM	224
QY	237	GESSVIDEH	EPWLTLMGL	254	
Db	225	IKHEIFDE	---LTIKGV	239	

RESULT 15

083446	PRELIMINARY;	PRT;	273 AA.
AC	083446;		
DT	01-NOV-1998 (TREMBLrel. 08, Created)		
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)		
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)		
DE	Hypothetical protein TP0431.		
GN	TP0431.		
OS	Treponema pallidum.		
OC	Bacteria; Spirochaetales; Spirochaetaceae; Treponema.		
OX	NCBI_TaxID=160;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-NICHOLS;		
RX	MEDLINE=98332770; PubMed=9665876;		
RA	Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,		
RA	Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,		
RA	Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,		
RA	Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,		
RA	McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,		
RA	Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,		
RA	Venter J.C.;		
RT	"Complete genome sequence of Treponema pallidum, the syphilis		
RT	spirochete.";		
RL	Science 281:375-388(1998).		
DR	EMBL; AE001220; AAC65417.1; .		
DR	TIGR; TP0431; .		
DR	InterPro; IPR004619; Baf.		
DR	Pfam; PF03309; Bvg_acc_factor; 1.		
DR	TIGRFAMS; TIGR00671; baf; 1.		
KW	Hypothetical protein; Complete proteome.		
SO	SEQUENCE 273 AA; 28472 MW; 439C9C77CB598BC0 CRC64;		

Query Match	21.7%	Score	291.5;	DB	16;	Length	273;
Best Local Similarity	33.1%;	Pred.	No. 2.7e-13;				
Matches	89;	Conservative	47;	Mismatches	108;	Indels	25;
							Gaps
							9;
QY	2	LLTIDVGNTHTVLGFDCED	-----IVEHWRISTDSRRTADELAVLLQGLMGHPLLGD	56			
Db	1	MLLIDVGNSHVFGI	-QGENGGRCVCRELFR LAPDARKTQDEYSLLIHALCERAGVGRAS	59			
QY	57	LGDGIDGIAICATVPSVLHELREVT	RRYYGDVPAVLVEPGVKTVPI	114			
Db	60	LRDAF	----ISSVVPVLTKTIADAVAQISG-VQPVVFGPWAYEHL	114			
QY	115	RIINAAVELYGGPAIVVDFGTATT	FDVAVSARGEYIGGVIAPGIEISVEALGVKGAQLR	174			
Db	115	LVANAAAYVHFRSACVVVDCGTALT	FTAVDGTGLIQGVAIAPGLRTAVQSLHTGTGAQLP	174			
QY	175	KIEVARPRSVIGKNTVEAMQSGI	VYGFAGQVDGVVNRMARELADDPDVTVIATGGLAPM	234			
Db	175	LVPLALPDSVLGKDTTHAVQAGV	VRGTLFVIRAMIAOCQKELG---CRCAAVITGGLSRL	231			
QY	235	VLGESSVID--EHEPWLTLMGL	----RLV	257			
Db	232	F---SSEVDFPPIDAQLTSLG	LAIARLV	257			

Search completed: June 24, 2003, 21:59:16
Job time : 23.6135 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 24, 2003, 22:24:12 ; Search time 14.2826 Seconds
(without alignments)
1947.059 Million cell updates/sec

Title: US-09-813-453A-53
Perfect score: 1303
Sequence: 1 MRLVVDIGNTSTTLAIFTGD.....VIDELAVLRGSDLLRMNMP 257

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 417779 seqs, 108206813 residues

Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1303	100.0	257	9	US-09-813-453A-53
2	322	24.7	254	9	US-09-813-453A-47
3	319	24.5	258	9	US-09-813-453A-2
4	316	24.3	262	9	US-09-813-453A-45
5	305	23.4	258	9	US-09-813-453A-49
6	301	23.1	255	9	US-09-813-453A-7
7	295	22.6	265	9	US-09-813-453A-4
8	274.5	21.1	272	9	US-09-813-453A-5
9	273.5	21.0	233	9	US-09-813-453A-17
10	271.5	20.8	272	9	US-09-712-363-276
11	265.5	20.4	219	9	US-09-813-453A-57
12	265	20.3	258	9	US-09-813-453A-6
13	261	20.0	260	9	US-09-813-453A-51
14	254.5	19.5	256	9	US-09-813-453A-55
15	253.5	19.5	262	9	US-09-813-453A-8
16	229.5	17.6	250	9	US-09-813-453A-3
17	228.5	17.5	246	9	US-09-813-453A-9
18	227	17.4	241	9	US-09-813-453A-63
19	225	17.3	229	9	US-09-813-453A-12

20	221	17.0	244	9	US-09-813-453A-41	Sequence 41, Appl
21	214	16.4	212	9	US-09-813-453A-59	Sequence 59, Appl
22	197.5	15.2	273	9	US-09-813-453A-10	Sequence 10, Appl
23	166.5	12.8	262	9	US-09-813-453A-11	Sequence 11, Appl
24	162.5	12.5	592	9	US-09-813-453A-43	Sequence 43, Appl
25	161.5	12.4	460	9	US-09-813-453A-39	Sequence 39, Appl
26	159.5	12.2	592	9	US-09-813-453A-22	Sequence 22, Appl
27	157	12.0	248	9	US-09-813-453A-20	Sequence 20, Appl
28	153.5	11.8	249	9	US-09-813-453A-70	Sequence 70, Appl
29	146.5	11.2	257	9	US-09-813-453A-13	Sequence 13, Appl
30	144	11.1	242	9	US-09-813-453A-65	Sequence 65, Appl
31	136.5	10.5	267	9	US-09-813-453A-15	Sequence 15, Appl
32	130.5	10.0	249	9	US-09-813-453A-61	Sequence 61, Appl
33	108	8.3	209	9	US-09-813-453A-21	Sequence 21, Appl
34	105.5	8.1	223	9	US-09-895-913A-74	Sequence 74, Appl
35	105.5	8.1	223	9	US-09-813-453A-14	Sequence 14, Appl
36	105.5	8.1	223	9	US-09-813-453A-67	Sequence 67, Appl
37	98	7.5	787	10	US-09-205-448-8	Sequence 8, Appl
38	84	6.4	574	9	US-09-764-868-774	Sequence 774, App
39	83.5	6.4	568	10	US-09-815-242-5140	Sequence 5140, Ap
40	82	6.3	831	10	US-09-815-242-10520	Sequence 10520, A
41	80.5	6.2	491	9	US-09-738-626-4429	Sequence 4429, Ap
42	80.5	6.2	491	12	US-10-024-370-3	Sequence 3, Appl
43	80	6.1	5877	9	US-10-142-515-11	Sequence 11, Appl
44	80	6.1	5935	9	US-10-243-243A-8	Sequence 8, Appl
45	79	6.1	991	9	US-10-231-353-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1

US-09-813-453A-53
; Sequence 53, Application US/09813453A
; Patent No. US20020168681A1
; GENERAL INFORMATION:
; APPLICANT: Yocum, R. Rogers
; APPLICANT: Patterson, Thomas A.
; TITLE OF INVENTION: MICROORGANISMS AND ASSAYS FOR THE IDENTIFICATION OF
; TITLE OF INVENTION: ANTIBIOTICS
; FILE REFERENCE: OGZ-001
; CURRENT APPLICATION NUMBER: US/09/813,453A
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/227,860
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 09/667,569
; PRIOR FILING DATE: 2000-09-21
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 53
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Chlorobium tepidum
US-09-813-453A-53

Query Match

Best Local Similarity 100.0%; Score 1303; DB 9; Length 257;
Matches 257; Conservative 0; Mismatches 0; Gaps 0;

QY	1	MRLVVDIGNTSTTLAIFTGDEEPSVESVPSALFADSTMTREVFGNMARKHGEPOAIAICS	50
DB	1	MRLVVDIGNTSTTLAIFTGDEEPSVESVPSALFADSTMTREVFGNMARKHGEPOAIAICS	60
QY	61	VVPSATAVGSALLESLFSVPLTICCKLRFPRLDYATPHTFGADRLALCAWSKHLFSEK	120
DB	61	VVPSATAVGSALLESLFSVPLTICCKLRFPRLDYATPHTFGADRLALCAWSKHLFSEK	120
QY	121	PVIAVDIGTAITFDVLDVTGNRYGGLIMPIDMAGALHSRTAQLPQVRIDRPSLLGRS	180
DB	121	PVIAVDIGTAITFDVLDVTGNRYGGLIMPIDMAGALHSRTAQLPQVRIDRPSLLGRS	180
QY	181	TTECIKSGVFWGVKQIGGLVDAIRGLDVRDFGSEVIVTGGNSRIIVPEIGPVSVID	240

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OM protein - protein search...
Run on: June 24, 2003, 22:08:46.3 Search time 11.9453 Seconds
(without alignments)
2373.336 Million cell updates/sec

Title: US-09-813-453A-11
Perfect score: 1331
Sequence: 1 MNKPLLSLLIIDIIGNTSIAFALFKDQVNLFIKMTNLMRLYDEVYSFFFEENFDFNVKV 262

Scoring table: BLOSUM62
Gapop: 10.0, Gapext 0.5

Searched: 417779 seqs, 108206813 residues

Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1331	100.0	262	9	US-09-813-453A-11
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3	276.5	20.8	262	9	US-09-813-453A-45
4	275.5	20.7	254	9	US-09-813-453A-47
5	271.5	20.4	258	9	US-09-813-453A-2
6	266.5	20.0	255	9	US-09-813-453A-7
7	262	19.7	250	9	US-09-813-453A-3
8	256.5	19.3	258	9	US-09-813-453A-49
9	231.5	17.4	233	9	US-09-813-453A-17
10	203	15.3	246	9	US-09-813-453A-9
11	197.5	14.8	258	9	US-09-813-453A-6
12	190	14.3	219	9	US-09-813-453A-57
13	189.5	14.2	260	9	US-09-813-453A-51
14	181.5	13.6	265	9	US-09-813-453A-4
15	170	12.8	273	9	US-09-813-453A-10
16	166.5	12.5	257	9	US-09-813-453A-53
17	159	11.9	262	9	US-09-813-453A-8
18	141.5	10.6	229	9	US-09-813-453A-12
19	138	10.4	272	9	US-09-712-363-276

20	138	10.4	272	9	US-09-813-453A-5	Sequence 5, Appl
21	136	10.2	241	9	US-09-813-453A-63	Sequence 63, Appl
22	135	10.1	244	9	US-09-813-453A-41	Sequence 41, Appl
23	121.5	9.1	209	9	US-09-813-453A-21	Sequence 21, Appl
24	121.5	9.1	476	10	US-09-774-414-3	Sequence 3, Appl
25	111	8.3	212	9	US-09-813-453A-59	Sequence 59, Appl
26	100	7.5	592	9	US-09-813-453A-43	Sequence 43, Appl
27	99.5	7.5	410	10	US-09-845-335-2	Sequence 2, Appl
28	96	7.2	592	9	US-09-813-453A-22	Sequence 22, Appl
29	93.5	7.0	242	9	US-09-813-453A-65	Sequence 65, Appl
30	92	6.9	460	9	US-09-813-453A-39	Sequence 39, Appl
31	92	6.9	1161	9	US-10-170-102-4	Sequence 4, Appl
32	90	6.8	257	9	US-09-813-453A-13	Sequence 13, Appl
33	88.5	6.6	223	9	US-09-895-913A-74	Sequence 74, Appl
34	88.5	6.6	223	9	US-09-813-453A-14	Sequence 14, Appl
35	88.5	6.6	223	9	US-09-813-453A-67	Sequence 67, Appl
36	88.5	6.6	370	9	US-10-106-698-6268	Sequence 6268, Ap
37	86.5	6.5	385	10	US-09-815-242-5713	Sequence 5713, Ap
38	86.5	6.5	518	10	US-09-815-242-12473	Sequence 12473, A
39	85.5	6.4	284	9	US-10-284-986-1	Sequence 1, Appl
40	85.5	6.4	284	10	US-09-846-808-1	Sequence 1, Appl
41	84.5	6.3	381	9	US-09-870-759-84	Sequence 84, Appl
42	84.5	6.3	1536	9	US-10-092-880-2	Sequence 2, Appl
43	84	6.3	401	10	US-09-815-242-5506	Sequence 5506, Ap
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45	83.5	6.3	248	9	US-09-813-453A-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1

US-09-813-453A-11
Sequence 11, Application US/09813453A
Patent No. US20020168681A1

GENERAL INFORMATION:

APPLICANT: Yocum, R. Rogers
APPLICANT: Patterson, Thomas A.
TITLE OF INVENTION: MICROORGANISMS AND ASSAYS FOR THE IDENTIFICATION OF
TITLE OF INVENTION: ANTIHISTOTICS
FILE REFERENCE: OGZ-001
CURRENT APPLICATION NUMBER: US/09/813,453A
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: US 60/227,860
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 09/667,569
PRIOR FILING DATE: 2000-09-21
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn ver. 2.0
SEQ ID NO 11
LENGTH: 262
TYPE: PRT
ORGANISM: Borrelia burgdorferi

US-09-813-453A-11

Query Match 100.0%; Score 131; DB 9; Length 262
Best Local Similarity 100.0%; Pred. No. 5.1e-115;
Matches 262; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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DB	1	MNKP	LLSE	LIID	IGNT	SI	AFAL	FKDN	QVNL	FIKMT	NLMRL	YDEV	YSFFE	ENFDF	NVKV	60		
QY	61	FISS	VPIL	NETK	NVIFS	FFKIK	PLFI	GF	DL	NYDL	TNPY	KSDK	FL	LGSD	VFANL	VAAL	120	
DB	61	FISS	VPIL	NETK	NVIFS	FFKIK	PLFI	GF	DL	NYDL	TNPY	KSDK	FL	LGSD	VFANL	VAAL	120	
QY	121	ENYS	FENV	LV	DLGT	ACTIF	AVSR	QD	GILG	GI	INS	GPL	NFNS	LLDN	AYLI	KKFP	ISTPN	180
DB	121	ENYS	FENV	LV	DLGT	ACTIF	AVSR	QD	GILG	GI	INS	GPL	NFNS	LLDN	AYLI	KKFP	ISTPN	180
QY	181	NLL	ERTT	SG	SVNS	GLFY	QYKY	LIEG	VYRDI	KQYK	KKFN	LITG	GNAD	LILS	LIE	IEFI	F	240

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protein - protein search, using sw model

Run on: June 24, 2003, 22:08:46 ; Search time 11.1246 Seconds
(without alignments)
2373.336 Million cell updates/sec

Title: US-09-813-453A-41
Perfect score: 1229
Sequence: 1 MSFNLIYDQNSACKVAFVR.....ILIHPLDVLGLNRLILEYV 244

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 417779 seqs, 108206813 residues

Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1229	100.0	244	9	US-09-813-453A-41
2	224	18.2	258	9	US-09-813-453A-6
3	221	18.0	257	9	US-09-813-453A-53
4	210.5	17.1	258	9	US-09-813-453A-49
5	208	16.9	255	9	US-09-813-453A-7
6	207.5	16.9	262	9	US-09-813-453A-45
7	207	16.8	258	9	US-09-813-453A-2
8	205.5	16.7	265	9	US-09-813-453A-4
9	201.5	16.4	256	9	US-09-813-453A-55
10	198	16.1	260	9	US-09-813-453A-51
11	197.5	16.1	254	9	US-09-813-453A-47
12	195.5	15.9	248	9	US-09-813-453A-20
13	184	15.0	219	9	US-09-813-453A-57
14	183.5	14.9	241	9	US-09-813-453A-63
15	181.5	14.8	242	9	US-09-813-453A-65
16	181	14.7	249	9	US-09-813-453A-61
17	178	14.5	249	9	US-09-813-453A-70
18	175.5	14.3	233	9	US-09-813-453A-17
19	174	14.2	212	9	US-09-813-453A-59

20	172.5	14.0	273	9	US-09-813-453A-10
21	167.5	13.6	250	9	US-09-813-453A-3
22	166	13.5	460	9	US-09-813-453A-39
23	163	13.3	267	9	US-09-813-453A-15
24	162	13.2	246	9	US-09-813-453A-9
25	161	13.1	592	9	US-09-813-453A-43
26	156	12.7	592	9	US-09-813-453A-22
27	153	12.4	272	9	US-09-712-363-276
28	153	12.4	272	9	US-09-813-453A-5
29	152	12.4	257	9	US-09-813-453A-13
30	135	11.0	262	9	US-09-813-453A-11
31	132.5	10.8	229	9	US-09-813-453A-12
32	131	10.7	262	9	US-09-813-453A-8
33	129.5	10.5	223	9	US-09-895-913A-74
34	129.5	10.5	223	9	US-09-813-453A-14
35	129.5	10.5	223	9	US-09-813-453A-67
36	126.5	10.3	209	9	US-09-813-453A-21
37	95.5	7.8	468	10	US-09-815-242-5530
38	95.5	7.8	468	10	US-09-815-242-12355
39	95.5	7.8	468	10	US-09-815-242-12934
40	91.5	7.4	783	9	US-09-738-626-5017
41	86	7.0	650	9	US-09-993-241-2
42	86	7.0	650	10	US-09-993-038-2
43	86	7.0	653	9	US-10-206-443-2
44	86	7.0	1140	9	US-09-974-973-19
45	86	7.0	1140	9	US-09-738-626-4265

ALIGNMENTS

RESULT 1

US-09-813-453A-41
; Sequence 41, Application US/09813453A
; Patent No. US20020168681A1
; GENERAL INFORMATION:
; APPLICANT: Yocum, R. Rogers
; APPLICANT: Patterson, Thomas A.
; TITLE OF INVENTION: MICROORGANISMS AND ASSAYS FOR THE IDENTIFICATION OF
; TITLE OF INVENTION: ANTIBIOTICS
; FILE REFERENCE: OGZ-001
; CURRENT APPLICATION NUMBER: US/09/813,453A
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/227,860
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 09/667,569
; PRIOR FILING DATE: 2000-09-21
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 41
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-09-813-453A-41

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Db	61	EAEAIYRSCAAASLMGMGTETPVPLRLQYDRRTLGDRLAAVVGHAHSLYPNTLLVIDAGT	120	
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Db	121	AITYERVSAEGIYLGNNISPLHRLFKALHFTGRPLIDPSGISPKIAEYGSSTEEAIT	180	
QY	181	AGVIHGLAGEIDRYDDLHAKEGRSVILTTGGDANYLARIIRSGILIHPLDVLGLNRL	240	
Db	181	AGVIHGLAGEIDRYDDLHAKEGRSVILTTGGDANYLARIIRSGILIHPLDVLGLNRL	240	

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OM protein - protein search, using sw model

Run on: June 24, 2003, 22:08:46 ; Search time 12.1733 Seconds
(without alignments)
2373.336 Million cell updates/sec

Title: US-09-813-453A-15
Perfect score: 1392
Sequence: 1 MIILDSGNSRLKVGWFDPD.....LDSPLDGLAALAAQGAPTA 267

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 417779 seqs, 108206813 residues
Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications_AA:*
- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
 - 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
 - 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
 - 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
 - 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
 - 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
 - 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
 - 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
 - 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
 - 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1392	100.0	267	9	US-09-813-453A-15
2	258.5	18.6	460	9	US-09-813-453A-39
3	256.5	18.4	592	9	US-09-813-453A-22
4	254.5	18.3	592	9	US-09-813-453A-43
5	194.5	14.0	242	9	US-09-813-453A-65
6	178.5	12.8	248	9	US-09-813-453A-20
7	163	11.7	244	9	US-09-813-453A-41
8	163	11.7	249	9	US-09-813-453A-61
9	154.5	11.1	241	9	US-09-813-453A-63
10	152	10.9	246	9	US-09-813-453A-9
11	148	10.6	255	9	US-09-813-453A-7
12	141	10.1	250	9	US-09-813-453A-3
13	140.5	10.1	258	9	US-09-813-453A-49
14	138	9.9	212	9	US-09-813-453A-59
15	138	9.9	262	9	US-09-813-453A-45
16	136.5	9.8	257	9	US-09-813-453A-53
17	134.5	9.7	260	9	US-09-813-453A-51
18	134	9.6	258	9	US-09-813-453A-6
19	134	9.6	265	9	US-09-813-453A-4

20	132	9.5	249	9	US-09-813-453A-70
21	131.5	9.4	254	9	US-09-813-453A-47
22	130.5	9.4	219	9	US-09-813-453A-57
23	129.5	9.3	258	9	US-09-813-453A-2
24	127.5	9.2	256	9	US-09-813-453A-55
25	125	9.0	233	9	US-09-813-453A-17
26	105	7.5	5215	9	US-09-860-846-2
27	105	7.5	5215	9	US-09-988-384B-2
28	105	7.5	5215	9	US-09-836-821-2
29	105	7.5	5215	10	US-09-861-289-2
30	103.5	7.4	262	9	US-09-813-453A-8
31	102.5	7.4	442	9	US-09-464-099A-64
32	102.5	7.4	442	9	US-10-214-766-36
33	102.5	7.4	442	10	US-09-861-696-64
34	97	7.0	257	9	US-09-813-453A-13
35	97	7.0	562	9	US-09-712-363-254
36	95	6.8	408	9	US-09-738-626-5136
37	94.5	6.8	437	9	US-10-145-415-101
38	92.5	6.6	272	9	US-09-712-363-276
39	92.5	6.6	272	9	US-09-813-453A-5
40	90.5	6.5	891	9	US-09-976-059-18
41	89.5	6.4	259	10	US-09-820-893-87
42	89.5	6.4	442	10	US-09-749-728B-11
43	89	6.4	4150	9	US-09-808-880-2
44	88.5	6.4	190	10	US-09-764-864-1071
45	88.5	6.4	1023	9	US-09-893-519A-14

ALIGNMENTS

RESULT 1

US-09-813-453A-15
; Sequence 15, Application US/09813453A
; Patent No. US20020168681A1
; GENERAL INFORMATION:
; APPLICANT: Yocum, R. Rogers
; APPLICANT: Patterson, Thomas A.
; TITLE OF INVENTION: MICROORGANISMS AND ASSAYS FOR THE IDENTIFICATION OF ANTIBIOTICS
; FILE REFERENCE: OGZ-001
; CURRENT APPLICATION NUMBER: US/09/813,453A
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/227,860
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 09/667,569
; PRIOR FILING DATE: 2000-09-21
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Bordetella pertussis
US-09-813-453A-15

Query Match 100.0%; Score 1392; DB 9; Length 267;
Best Local Similarity 100.0%; Pred. No. 3.2e-114;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MIILDSGNSRLKVGWFDPDQAAREPAPVAFDNLDLALGRWLATLPRRQALGVNV	60
Db	1	MIILDSGNSRLKVGWFDPDQAAREPAPVAFDNLDLALGRWLATLPRRQALGVNV	50
QY	61	AGLARGEIAATLRAGGCDIRWLRAQPLAMGLRNGYRNPDLGADRWACMVGVLARQPSV	120
Db	61	AGLARGEIAATLRAGGCDIRWLRAQPLAMGLRNGYRNPDLGADRWACMVGVLARQPSV	120
QY	121	HPLLVASFGTATTLDTIGDPNVFPFGLILPGPAMRGALAYTAHLPLADGLVADYPID	180
Db	121	HPLLVASFGTATTLDTIGDPNVFPFGLILPGPAMRGALAYTAHLPLADGLVADYPID	180
QY	181	THQAIASGIAAQAQATVROWLAGRORYGOAPEIYVAGGWNPEVROEAERLLAVTGAIFG	240
Db	181	THQAIASGIAAQAQATVROWLAGRORYGOAPEIYVAGGWNPEVROEAERLLAVTGAIFG	240

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- protein search, using sw model

June 24, 2003, 22:24:12 ; Search time 11.7818 Seconds
(without alignments)
1947.059 Million cell updates/sec

Title: US-09-813-453A-59
Perfect score: 1077
Sequence: 1 MTQHFLFDIGNTVKIGIA.....SLNHGFIQFAAMTEGVLA 212

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 417779 seqs, 108206813 residues
Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1077	100.0	212	9	US-09-813-453A-59	Sequence 59, Appl
2	379.5	35.2	262	9	US-09-813-453A-45	Sequence 45, Appl
3	352.5	32.7	258	9	US-09-813-453A-49	Sequence 49, Appl
4	348.5	32.4	219	9	US-09-813-453A-57	Sequence 57, Appl
5	338.5	31.4	233	9	US-09-813-453A-17	Sequence 17, Appl
6	338.5	31.4	255	9	US-09-813-453A-7	Sequence 7, Appl
7	338.5	31.4	258	9	US-09-813-453A-2	Sequence 2, Appl
8	330.5	30.7	254	9	US-09-813-453A-47	Sequence 47, Appl
9	327.5	30.4	250	9	US-09-813-453A-3	Sequence 3, Appl
10	315.5	29.3	256	9	US-09-813-453A-55	Sequence 55, Appl
11	307.5	28.6	260	9	US-09-813-453A-51	Sequence 51, Appl
12	280	26.0	265	9	US-09-813-453A-4	Sequence 4, Appl
13	271	25.2	262	9	US-09-813-453A-8	Sequence 8, Appl
14	240.5	22.3	258	9	US-09-813-453A-6	Sequence 6, Appl
15	221	20.5	246	9	US-09-813-453A-9	Sequence 9, Appl
16	214	19.9	257	9	US-09-813-453A-53	Sequence 53, Appl
17	209.5	19.5	272	9	US-09-712-363-276	Sequence 276, App
18	209.5	19.5	272	9	US-09-813-453A-5	Sequence 5, Appl
19	192.5	17.9	273	9	US-09-813-453A-10	Sequence 10, Appl

20	180.5	16.8	241	9	US-09-813-453A-63	Sequence 63, Appl
21	174	16.2	244	9	US-09-813-453A-41	Sequence 41, Appl
22	138	12.8	267	9	US-09-813-453A-15	Sequence 15, Appl
23	136.5	12.7	592	9	US-09-813-453A-43	Sequence 43, Appl
24	134	12.4	249	9	US-09-813-453A-70	Sequence 70, Appl
25	133.5	12.4	460	9	US-09-813-453A-39	Sequence 39, Appl
26	132.5	12.3	592	9	US-09-813-453A-22	Sequence 22, Appl
27	120.5	11.2	229	9	US-09-813-453A-12	Sequence 12, Appl
28	114.5	10.6	249	9	US-09-813-453A-61	Sequence 61, Appl
29	111	10.3	262	9	US-09-813-453A-11	Sequence 11, Appl
30	107	9.9	248	9	US-09-813-453A-20	Sequence 20, Appl
31	104	9.7	242	9	US-09-813-453A-65	Sequence 65, Appl
32	102	9.5	223	9	US-09-895-913A-74	Sequence 74, Appl
33	102	9.5	223	9	US-09-813-453A-14	Sequence 14, Appl
34	102	9.5	223	9	US-09-813-453A-67	Sequence 67, Appl
35	92.5	8.6	257	9	US-09-813-453A-13	Sequence 13, Appl
36	88	8.2	275	9	US-10-106-698-6389	Sequence 6389, Ap
37	85	7.9	209	9	US-09-813-453A-21	Sequence 21, Appl
38	82.5	7.7	486	10	US-09-801-368-154	Sequence 154, App
39	82	7.6	250	9	US-10-167-015-2	Sequence 2, Appl
40	81	7.5	376	9	US-09-738-626-6189	Sequence 6189, Ap
41	80.5	7.5	2201	12	US-10-029-907-3	Sequence 3, Appl
42	79.5	7.4	674	9	US-10-086-464-14	Sequence 14, Appl
43	79	7.3	324	10	US-09-815-242-5117	Sequence 5117, Ap
44	77	7.1	4999	9	US-09-976-059-15	Sequence 15, Appl
45	76	7.1	731	9	US-10-086-464-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-09-813-453A-59
; Sequence 59, Application US/09813453A
; Patent No. US20020168681A1
; GENERAL INFORMATION:
; APPLICANT: Yocum, R. Rogers
; APPLICANT: Patterson, Thomas A.
; TITLE OF INVENTION: MICROORGANISMS AND ASSAYS FOR THE IDENTIFICATION OF
; TITLE OF INVENTION: ANTIBIOTICS
; FILE REFERENCE: OGZ-001
; CURRENT APPLICATION NUMBER: US/09/813,453A
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/227,860
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 09/667,569
; PRIOR FILING DATE: 2000-09-21
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Desulfovibrio vulgaris
US-09-813-453A-59

Query Match 100.0%; Score 1077; DB 9; Length 212;
Best Local Similarity 100.0%; Pred. No. 1e-102;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MTQHFLFDIGNTVKIGIAVETAVLT	SYVLPDTPGQTTDSIGLRLLLEVL	RHAGLGPADV	60
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QY	61	GACVASSVVP	GVNPLIRACERYLYRKLLEFAPGDIA	PLDNRYP	EAEGADRLVAAYAA 120
Db	61	GACVASSVVP	GVNPLIRACERYLYRKLLEFAPGDIA	PLDNRYP	EAEGADRLVAAYAA 120
QY	121	RRLYPGRSLV	SVDFGTATTDFDCVEGGAYLGG	LICPGVLSSAGALSSRTAKLPRISLEVE	180
Db	121	RRLYPGRSLV	SVDFGTATTDFDCVEGGAYLGG	LICPGVLSSAGALSSRTAKLPRISLEVE	180
QY	181	EDSPVIGRSTT	SLNHGFIQFAAMTEGVLA 212		

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GenCore version 5.1.6
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protein - protein search, using sw model

Run on: June 24, 2003, 22:24:12 ; Search time 13.449 Seconds
(without alignments)
1947.059 Million cell updates/sec

Title: US-09-813-453A-65
Perfect score: 1230
Sequence: 1 MNDWLFDLGNSRFKASLRE.....HRPTLVLDGLAIWAAVAAV 242

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 417779 seqs, 108206813 residues
Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB pep.*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB pep.*
7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1230	100.0	242	9	US-09-813-453A-65
2	200	16.3	592	9	US-09-813-453A-43
3	199.5	16.2	460	9	US-09-813-453A-39
4	198.5	16.1	592	9	US-09-813-453A-22
5	194.5	15.8	267	9	US-09-813-453A-15
6	193	15.7	248	9	US-09-813-453A-20
7	181.5	14.8	244	9	US-09-813-453A-41
8	168.5	13.7	249	9	US-09-813-453A-61
9	165.5	13.5	249	9	US-09-813-453A-70
10	144	11.7	257	9	US-09-813-453A-53
11	143.5	11.7	219	9	US-09-813-453A-57
12	143.5	11.7	241	9	US-09-813-453A-63
13	140.5	11.4	260	9	US-09-813-453A-51
14	139	11.3	265	9	US-09-813-453A-4
15	134.5	10.9	258	9	US-09-813-453A-2
16	128.5	10.4	262	9	US-09-813-453A-8
17	128	10.4	255	9	US-09-813-453A-7
18	125.5	10.2	258	9	US-09-813-453A-6
19	120	9.8	256	9	US-09-813-453A-55

20	117	9.5	262	9	US-09-813-453A-45	Sequence 45, Appl
21	116	9.4	233	9	US-09-813-453A-17	Sequence 17, Appl
22	115.5	9.4	223	9	US-09-895-913A-74	Sequence 74, Appl
23	115.5	9.4	223	9	US-09-813-453A-14	Sequence 14, Appl
24	115.5	9.4	223	9	US-09-813-453A-67	Sequence 67, Appl
25	115	9.3	258	9	US-09-813-453A-49	Sequence 49, Appl
26	112	9.1	272	9	US-09-712-363-276	Sequence 276, App
27	112	9.1	272	9	US-09-813-453A-5	Sequence 5, Appl
28	108.5	8.8	250	9	US-09-813-453A-3	Sequence 3, Appl
29	107.5	8.7	254	9	US-09-813-453A-47	Sequence 47, Appl
30	105	8.5	498	10	US-09-815-242-11777	Sequence 11777, A
31	104	8.5	212	9	US-09-813-453A-59	Sequence 59, Appl
32	103	8.4	246	9	US-09-813-453A-9	Sequence 9, Appl
33	99	8.0	257	9	US-09-813-453A-13	Sequence 13, Appl
34	95	7.7	229	9	US-09-813-453A-12	Sequence 12, Appl
35	93.5	7.6	262	9	US-09-813-453A-11	Sequence 11, Appl
36	93.5	7.6	323	10	US-09-815-242-13734	Sequence 13734, A
37	93.5	7.6	4999	9	US-09-976-059-15	Sequence 15, Appl
38	89.5	7.3	209	9	US-09-813-453A-21	Sequence 21, Appl
39	88	7.2	273	9	US-09-813-453A-10	Sequence 10, Appl
40	81.5	6.6	653	10	US-09-759-010-2	Sequence 2, Appl
41	81.5	6.6	654	9	US-09-919-039-260	Sequence 260, App
42	81.5	6.6	654	10	US-09-919-172-54	Sequence 54, Appl
43	81.5	6.6	4999	9	US-09-976-059-14	Sequence 14, Appl
44	80.5	6.5	323	10	US-09-815-242-10321	Sequence 10321, A
45	80.5	6.5	342	9	US-09-712-363-210	Sequence 210, App

ALIGNMENTS

RESULT 1

US-09-813-453A-65
; Sequence 65, Application US/09813453A
; Patent No. US20020168681A1

GENERAL INFORMATION:

; APPLICANT: Yocum, R. Rogers
; APPLICANT: Patterson, Thomas A.
; TITLE OF INVENTION: MICROORGANISMS AND ASSAYS FOR THE IDENTIFICATION OF
; TITLE OF INVENTION: ANTIBIOTICS
; FILE REFERENCE: OG2-001
; CURRENT APPLICATION NUMBER: US/09/813,453A
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/227,860
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 09/667,569
; PRIOR FILING DATE: 2000-09-21
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Xylella fastidiosa

US-09-813-453A-65	Query Match	100.0%;	Score 1230;	DB 9;	Length 242;
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	Matches 242;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MNDWLFDLGNSRFKASLREGVIGPVTVLPYLTTETMDAFALQELPRGRVAYLASVAAPAI	60		
DB	1	MNDWLFDLGNSRFKASLREGVIGPVTVLPYLTTETMDAFALQELPRGRVAYLASVAAPAI	60		
QY	61	TTHTVLEVLKIHFEQVQVAATAACAGVRIAYAHPRFVGDRFLALLGSYGEGNVLVGVG	120		
DB	61	TTHTVLEVLKIHFEQVQVAATAACAGVRIAYAHPRFVGDRFLALLGSYGEGNVLVGVG	120		
QY	121	TALTIDLLAANGCHLGGKRISASPTLMRQALHARAEQLPLSGGNYLEFAEDTEDALVSGCN	180		
DB	121	TALTIDLLAANGCHLGGKRISASPTLMRQALHARAEQLPLSGGNYLEFAEDTEDALVSGCN	180		
QY	181	GAVALIERSLYEAHQRLDQSVRLLLHGGGVASLLPWLGDVVHRTLVLDGLAIWAAVAA	240		
DB	181	GAVALIERSLYEAHQRLDQSVRLLLHGGGVASLLPWLGDVVHRTLVLDGLAIWAAVAA	240		

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protein - protein search, using sw model

Run on: June 24, 2003, 22:24:12 ; Search time 12.3931 Seconds
(without alignments)
1947.059 Million cell updates/sec

Title: US-09-813-453A-67
Perfect score: 1153
Sequence: 1 MPARQSFTDLKLVLCIDGN.....RLVFDGMEIALKAGILECK 223

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 417779 seqs, 108206813 residues
Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications_AA:*
- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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 - 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
 - 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
 - 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1153	100.0	223	9	US-09-813-453A-74
2	1153	100.0	223	9	US-09-813-453A-14
3	1153	100.0	223	9	US-09-813-453A-67
4	391.5	34.0	209	9	US-09-813-453A-21
5	165	14.3	246	9	US-09-813-453A-9
6	159.5	13.8	248	9	US-09-813-453A-20
7	148	12.8	249	9	US-09-813-453A-70
8	144.5	12.5	241	9	US-09-813-453A-63
9	144.5	12.5	249	9	US-09-813-453A-61
10	141.5	12.3	257	9	US-09-813-453A-13
11	138.5	12.0	229	9	US-09-813-453A-12
12	129.5	11.2	244	9	US-09-813-453A-41
13	116.5	10.1	592	9	US-09-813-453A-22
14	116.5	10.1	592	9	US-09-813-453A-43
15	116	10.1	460	9	US-09-813-453A-39
16	115.5	10.0	242	9	US-09-813-453A-65
17	109.5	9.5	233	9	US-09-813-453A-17
18	109.5	9.5	258	9	US-09-813-453A-2
19	108	9.4	219	9	US-09-813-453A-57

20	105.5	9.2	257	9	US-09-813-453A-53
21	102.5	8.9	250	9	US-09-813-453A-3
22	102	8.8	212	9	US-09-813-453A-59
23	101	8.8	256	9	US-09-813-453A-55
24	100.5	8.7	255	9	US-09-813-453A-7
25	98.5	8.5	262	9	US-09-813-453A-45
26	91	7.9	254	9	US-09-813-453A-47
27	89.5	7.8	272	9	US-09-712-363-276
28	89.5	7.8	272	9	US-09-813-453A-5
29	88.5	7.7	262	9	US-09-813-453A-11
30	87.5	7.6	258	9	US-09-813-453A-49
31	87	7.5	947	10	US-09-801-574-4
32	84	7.3	764	10	US-09-815-242-11556
33	82.5	7.2	265	9	US-09-813-453A-4
34	82	7.1	688	10	US-09-815-242-11416
35	81.5	7.1	273	9	US-09-813-453A-10
36	80	6.9	260	9	US-09-813-453A-51
37	79	6.9	310	10	US-09-815-242-10283
38	79	6.9	375	9	US-09-981-353-113
39	79	6.9	2799	9	US-10-151-736-4
40	78	6.8	770	9	US-10-153-668-7
41	77.5	6.7	258	9	US-09-813-453A-6
42	77	6.7	692	9	US-10-101-464A-897
43	76	6.6	434	9	US-10-153-668-454
44	76	6.6	439	9	US-09-374-046A-44
45	76	6.6	653	9	US-10-174-590-402

ALIGNMENTS

RESULT 1
US-09-895-913A-74
; Sequence 74, Application US/09895913A
; Patent No. US20020160456A1
; GENERAL INFORMATION:
; APPLICANT: Kleanthous, Harold
; APPLICANT: Al-Garawi, Amal
; APPLICANT: Miller, Charles
; APPLICANT: Tomb, Jean Francois
; APPLICANT: Oomen, Raymond P.
; TITLE OF INVENTION: Identification of Polynucleotides
; TITLE OF INVENTION: Encoding No. US20020160456A1 Helicobacter Polypeptides in t
; TITLE OF INVENTION: Genome
; FILE REFERENCE: 06132/043002
; CURRENT APPLICATION NUMBER: US/09/895,913A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 08/881,227
; PRIOR FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-895-913A-74

Query Match 100.0%; Score 1153; DB 9; Length 223;
Best Local Similarity 100.0%; Pred. No. 1.8e-107;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps

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DB	1	MPARQSFTDLKLVLCIDGNTRIHFQAQNYQLFSSAKEDLKRGLGIQKEIFYTSVNEENE
QY	61	LLNCYPNAKNIAGFFHLETDYVGLGIDROMACLAIVNGVVDAGSAITIDLIKFKGHLG
DB	61	LLNCYPNAKNIAGFFHLETDYVGLGIDROMACLAIVNGVVDAGSAITIDLIKFKGHLG
QY	121	CILPGLAQYIHAYKSAKILEQPFKALDSLEVLPKSTRDAVNYGMVLSVIACIQLAKNQ
DB	121	CILPGLAQYIHAYKSAKILEQPFKALDSLEVLPKSTRDAVNYGMVLSVIACIQLAKNQ

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GenCore version 5.1.6
Copyright (c) 1993 - 2003. Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 24, 2003, 22:08:46 ; Search time 10.1672 Seconds
(without alignments)
2373.336 Million cell updates/sec

Title: US-09-813-453A-14
Perfect score: 1153
Sequence: 1 MPARQSFTDLKLVLCIDGN.....RLVFDGMEIALKAGILECK 223

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 417779 seqs, 108206813 residues

Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1153	100.0	223	9	US-09-895-913A-74
2	1153	100.0	223	9	US-09-813-453A-14
3	1153	100.0	223	9	US-09-813-453A-67
4	391.5	34.0	209	9	US-09-813-453A-21
5	165	14.3	246	9	US-09-813-453A-9
6	159.5	13.8	248	9	US-09-813-453A-20
7	148	12.8	249	9	US-09-813-453A-70
8	144.5	12.5	241	9	US-09-813-453A-63
9	144.5	12.5	249	9	US-09-813-453A-61
10	141.5	12.3	257	9	US-09-813-453A-13
11	138.5	12.0	229	9	US-09-813-453A-12
12	129.5	11.2	244	9	US-09-813-453A-41
13	116.5	10.1	592	9	US-09-813-453A-22
14	116.5	10.1	592	9	US-09-813-453A-43
15	116	10.1	460	9	US-09-813-453A-39
16	115.5	10.0	242	9	US-09-813-453A-65
17	109.5	9.5	233	9	US-09-813-453A-17
18	109.5	9.5	258	9	US-09-813-453A-2
19	108	9.4	219	9	US-09-813-453A-57

20	105.5	9.2	257	9	US-09-813-453A-53	Sequence 53, Appl
21	102.5	8.9	250	9	US-09-813-453A-3	Sequence 3, Appl
22	102	8.8	212	9	US-09-813-453A-59	Sequence 59, Appl
23	101	8.8	256	9	US-09-813-453A-55	Sequence 55, Appl
24	100.5	8.7	255	9	US-09-813-453A-7	Sequence 7, Appl
25	98.5	8.5	262	9	US-09-813-453A-45	Sequence 45, Appl
26	91	7.9	254	9	US-09-813-453A-47	Sequence 47, Appl
27	89.5	7.8	272	9	US-09-712-363-276	Sequence 276, App
28	89.5	7.8	272	9	US-09-813-453A-5	Sequence 5, Appl
29	88.5	7.7	262	9	US-09-813-453A-11	Sequence 11, Appl
30	87.5	7.6	258	9	US-09-813-453A-49	Sequence 49, Appl
31	87	7.5	947	10	US-09-801-574-4	Sequence 4, Appl
32	84	7.3	764	10	US-09-815-242-11556	Sequence 11556, A
33	82.5	7.2	265	9	US-09-813-453A-4	Sequence 4, Appl
34	82	7.1	688	10	US-09-815-242-11416	Sequence 11416, A
35	81.5	7.1	273	9	US-09-813-453A-10	Sequence 10, Appl
36	80	6.9	260	9	US-09-813-453A-51	Sequence 51, Appl
37	79	6.9	310	10	US-09-815-242-10283	Sequence 10283, A
38	79	6.9	375	9	US-09-81-353-113	Sequence 113, App
39	79	6.9	2799	9	US-10-151-736-4	Sequence 4, Appl
40	78	6.8	770	9	US-10-153-668-7	Sequence 7, Appl
41	77.5	6.7	258	9	US-09-813-453A-6	Sequence 6, Appl
42	77	6.7	692	9	US-10-101-464A-897	Sequence 897, App
43	76	6.6	434	9	US-10-153-668-454	Sequence 454, App
44	76	6.6	439	9	US-09-374-046A-44	Sequence 44, Appl
45	76	6.6	653	9	US-10-174-590-402	Sequence 402, App

ALIGNMENTS

RESULT 1
US-09-895-913A-74
; Sequence 74, Application US/09895913A
; Patent No. US20020160456A1
; GENERAL INFORMATION:
; APPLICANT: Kleanthous, Harold
; APPLICANT: Al-Garawi, Amal
; APPLICANT: Miller, Charles
; APPLICANT: Tomb, Jean Francois
; APPLICANT: Oomen, Raymond P.
; TITLE OF INVENTION: Identification of polynucleotides
; TITLE OF INVENTION: Encoding No. US20020160456A1 Helicobacter P.
; TITLE OF INVENTION: Genome
; FILE REFERENCE: 06132/043002
; CURRENT APPLICATION NUMBER: US/09/895,913A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 08/881,227
; PRIOR FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-895-913A-74

Query Match 100.0%; Score 1153; DB 9; Length 223;
Best Local Similarity 100.0%; Pred. No. 1.8e-107;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MPARQSFTDLKLVLCIDIGNTRIHFACNYQLFSSAKEDLKRLGIQKEIFYISVNEENKA	60
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2	2223	93.2	592	9	US-09-813-453A-22	Sequence 22, Appl
3	2197	92.2	592	9	US-09-813-453A-43	Sequence 43, Appl
4	258.5	10.8	267	9	US-09-813-453A-15	Sequence 15, Appl
5	232.5	9.8	248	9	US-09-813-453A-20	Sequence 20, Appl
6	232	9.7	249	9	US-09-813-453A-61	Sequence 61, Appl
7	204	8.6	302	9	US-10-260-877-110	Sequence 110, App
8	199.5	8.4	242	9	US-09-813-453A-65	Sequence 65, Appl
9	185	7.8	260	9	US-09-813-453A-51	Sequence 51, Appl
10	179	7.5	265	9	US-09-813-453A-4	Sequence 4, Appl
11	177	7.4	249	9	US-09-813-453A-70	Sequence 70, Appl
12	169	7.1	250	9	US-09-813-453A-3	Sequence 3, Appl
13	168	7.0	262	9	US-09-813-453A-45	Sequence 45, Appl
14	166	7.0	244	9	US-09-813-453A-41	Sequence 41, Appl
15	161.5	6.8	257	9	US-09-813-453A-53	Sequence 53, Appl
16	153	6.4	219	9	US-09-813-453A-57	Sequence 57, Appl
17	153	6.4	288	9	US-09-738-626-4286	Sequence 4286, Ap
18	152.5	6.4	246	9	US-09-813-453A-9	Sequence 9, Appl
19	151	6.3	258	9	US-09-813-453A-2	Sequence 2, Appl

THE UNIVERSITY OF CHICAGO

RESULT 1

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GenCore version 5.1.6
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protein - protein search, using sw model

Run on: June 24, 2003, 22:08:46 ; Search time 26.9909 Seconds
(without alignments)
2373.336 Million cell updates/sec

Title: US-09-813-453A-22
Perfect score: 3080
Sequence: 1 MTVLKPSHWRVLAELADGLP.....LVTHGLNLIAAEGGESEHT 592

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 41779 seqs, 108206813 residues 417779
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3080	100.0	592	9 US-09-813-453A-22	Sequence 22, Appl
2	3024	98.2	592	9 US-09-813-453A-43	Sequence 43, Appl
3	2223	72.2	460	9 US-09-813-453A-39	Sequence 39, Appl
4	256.5	8.3	267	9 US-09-813-453A-15	Sequence 15, Appl
5	256	8.3	302	9 US-10-260-877-110	Sequence 110, Appl
6	243	7.9	249	9 US-09-813-453A-61	Sequence 61, Appl
7	231.5	7.5	248	9 US-09-813-453A-20	Sequence 20, Appl
8	198.5	6.4	242	9 US-09-813-453A-65	Sequence 65, Appl
9	187	6.1	249	9 US-09-813-453A-70	Sequence 70, Appl
10	183.5	6.0	288	9 US-09-738-626-4286	Sequence 4286, Ap
11	180.5	5.9	265	9 US-09-813-453A-4	Sequence 4, Appl1
12	179	5.8	311	10 US-09-859-270-2	Sequence 2, Appl1
13	175	5.7	260	9 US-09-813-453A-51	Sequence 51, Appl
14	168	5.5	250	9 US-09-813-453A-3	Sequence 3, Appl1
15	168	5.5	262	9 US-09-813-453A-45	Sequence 45, Appl
16	159.5	5.2	257	9 US-09-813-453A-53	Sequence 53, Appl
17	156	5.1	244	9 US-09-813-453A-41	Sequence 41, Appl
18	152	4.9	219	9 US-09-813-453A-57	Sequence 57, Appl
19	152	4.9	272	9 US-09-712-363-276	Sequence 276, App

20	152	4.9	272	9 US-09-813-453A-5	Sequence 5, Appl
21	150.5	4.9	246	9 US-09-813-453A-9	Sequence 9, Appl
22	150	4.9	258	9 US-09-813-453A-2	Sequence 2, Appl
23	147.5	4.8	273	9 US-09-813-453A-10	Sequence 10, Appl
24	146	4.7	258	9 US-09-813-453A-49	Sequence 49, Appl
25	141	4.6	255	9 US-09-813-453A-7	Sequence 7, Appl
26	141	4.6	257	9 US-09-813-453A-13	Sequence 13, Appl
27	140.5	4.6	256	9 US-09-813-453A-55	Sequence 55, Appl
28	140	4.5	258	9 US-09-813-453A-6	Sequence 6, Appl
29	137	4.4	254	9 US-09-813-453A-47	Sequence 47, Appl
30	133	4.3	233	9 US-09-813-453A-17	Sequence 17, Appl
31	132.5	4.3	212	9 US-09-813-453A-59	Sequence 59, Appl
32	116.5	3.8	223	9 US-09-895-913A-74	Sequence 74, Appl
33	116.5	3.8	223	9 US-09-813-453A-14	Sequence 14, Appl
34	116.5	3.8	223	9 US-09-813-453A-67	Sequence 67, Appl
35	115	3.7	3816	9 US-09-808-880-3	Sequence 3, Appl
36	112.5	3.7	241	9 US-09-813-453A-63	Sequence 63, Appl
37	112	3.6	472	10 US-09-815-242-13727	Sequence 13727, Appl
38	110	3.6	340	10 US-09-815-242-11743	Sequence 11743, Appl
39	108.5	3.5	286	9 US-09-769-787-100	Sequence 100, Appl
40	108	3.5	229	9 US-09-813-453A-12	Sequence 12, Appl
41	106.5	3.5	335	10 US-09-815-242-5138	Sequence 5138, Appl
42	105	3.4	1222	10 US-09-137-531-15	Sequence 15, Appl
43	105	3.4	1252	10 US-09-137-531-9	Sequence 9, Appl
44	104.5	3.4	4613	9 US-09-860-846-31	Sequence 31, Appl
45	104.5	3.4	4613	9 US-09-988-384B-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1
US-09-813-453A-22
; Sequence 22, Application US/09813453A
; Patent No. US20020168681A1
; GENERAL INFORMATION:
; APPLICANT: Yocum, R. Rogers
; APPLICANT: Patterson, Thomas A.
; TITLE OF INVENTION: MICROORGANISMS AND ASSAYS FOR THE IDENTIFICATION OF
; TITLE OF INVENTION: ANTIBIOTICS
; FILE REFERENCE: OGZ-001
; CURRENT APPLICATION NUMBER: US/09/813,453A
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/227,860
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 09/667,569
; PRIOR FILING DATE: 2000-09-21
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-813-453A-22

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Best Local Similarity	100.0%	Pred. No.	3.7e-251				
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Gap							
QY	1	MTVLKPSHWRVLAELADGLPQHVSQLARMADMKPQQLNGFWQMPAHIRGLLRQHDGY					
Db	1	MTVLKPSHWRVLAELADGLPQHVSQLARMADMKPQQLNGFWQMPAHIRGLLRQHDGY					
QY	61	LVRPLAVFDAEGLRELGERSGFQTALKHECASSNDEILELARIAPDKAHKTKICVTHLC					
Db	61	LVRPLAVFDAEGLRELGERSGFQTALKHECASSNDEILELARIAPDKAHKTKICVTHLC					
QY	121	GRGROGRKWSHRLGECIMFSGVWFDPRQYELGSLSPVAACRRALSRLGLKTKIKY					
Db	121	GRGROGRKWSHRLGECIMFSGVWFDPRQYELGSLSPVAACRRALSRLGLKTKIKY					
QY	181	DLVVGRDKLGGILLETVRTGGKTVAVVGGIGINFVLPKEVENAAASVLSLPQASRGN					
Db	181	DLVVGRDKLGGILLETVRTGGKTVAVVGGIGINFVLPKEVENAAASVLSLPQASRGN					

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protein search, using sw model

June 24, 2003, 22:08:46 ; Search time 26.9909 Seconds
(without alignments)
2373.336 Million cell updates/sec

Title: US-09-813-453A-43
Perfect score: 3078
Sequence: 1 MTVLKLSHWRVLAELADGLP.....LVYGLLNMAAGREYEH 592

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 417779 seqs, 108206813 residues

Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PTCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/PTCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3078	100.0	592	9	US-09-813-453A-43
2	3024	98.2	592	9	US-09-813-453A-22
3	2197	71.4	460	9	US-09-813-453A-39
4	259	8.4	302	9	US-10-260-877-110
5	254.5	8.3	267	9	US-09-813-453A-15
6	245	8.0	249	9	US-09-813-453A-61
7	234.5	7.6	248	9	US-09-813-453A-20
8	200	6.5	242	9	US-09-813-453A-65
9	194	6.3	311	10	US-09-859-270-2
10	191	6.2	249	9	US-09-813-453A-70
11	184.5	6.0	288	9	US-09-738-626-4286
12	177	5.8	265	9	US-09-813-453A-4
13	172	5.6	260	9	US-09-813-453A-51
14	169.5	5.5	262	9	US-09-813-453A-45
15	168	5.5	250	9	US-09-813-453A-3
16	162.5	5.3	257	9	US-09-813-453A-53
17	161	5.2	244	9	US-09-813-453A-41
18	150	4.9	219	9	US-09-813-453A-57
19	150	4.9	258	9	US-09-813-453A-2

20	147.5	4.8	272	9	US-09-712-363-276
21	147.5	4.8	272	9	US-09-813-453A-5
22	147.5	4.8	273	9	US-09-813-453A-10
23	146	4.7	246	9	US-09-813-453A-9
24	146	4.7	258	9	US-09-813-453A-49
25	141	4.6	257	9	US-09-813-453A-13
26	140.5	4.6	256	9	US-09-813-453A-55
27	139.5	4.5	255	9	US-09-813-453A-7
28	136.5	4.4	212	9	US-09-813-453A-59
29	136	4.4	254	9	US-09-813-453A-47
30	134	4.4	258	9	US-09-813-453A-6
31	133	4.3	233	9	US-09-813-453A-17
32	116.5	3.8	223	9	US-09-895-913A-74
33	116.5	3.8	223	9	US-09-813-453A-14
34	116.5	3.8	223	9	US-09-813-453A-67
35	115.5	3.8	241	9	US-09-813-453A-63
36	114.5	3.7	3816	9	US-09-808-880-3
37	105.5	3.4	4613	9	US-09-860-846-31
38	105.5	3.4	4613	9	US-09-988-384B-31
39	105.5	3.4	4613	9	US-09-836-821-31
40	105.5	3.4	4613	10	US-09-861-289-31
41	105.5	3.4	11877	9	US-09-860-846-6
42	105.5	3.4	11877	9	US-09-836-821-6
43	105.5	3.4	11877	10	US-09-861-289-6
44	105.5	3.4	12199	9	US-09-988-384B-6
45	104.5	3.4	340	10	US-09-815-242-11743

ALIGNMENTS

RESULT 1

US-09-813-453A-43
; Sequence 43, Application US/09813453A
; Patent No. US20020168681A1
; GENERAL INFORMATION:
; APPLICANT: Yocum, R. Rogers
; APPLICANT: Patterson, Thomas A.
; TITLE OF INVENTION: MICROORGANISMS AND ASSAYS FOR THE IDENTIFICATION OF
; TITLE OF INVENTION: ANTIBIOTICS
; FILE REFERENCE: OGZ-001
; CURRENT APPLICATION NUMBER: US/09/813,453A
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/227,860
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 09/667,569
; PRIOR FILING DATE: 2000-09-21
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Neisseria meningitidis

US-09-813-453A-43	Query Match	100.0%	Score 3078;	DB 9;	Length 592;
	Best Local Similarity	100.0%	Pred. No. 6.4e-257;		
	Matches 592;	Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;
QY	1	MTVLKLSHWRVLAELADGLPQHVSQLARMADMKPQQLNGFWQMPAHIRGLRQHDGYWR	60		
Db	1	MTVLKLSHWRVLAELADGLPQHVSQLARMADMKPQQLNGFWQMPAHIRGLRQHDGYWR	60		
QY	61	LVRPLAVFDAEGLRELGERSGFQTALKHECASSNDEILELARIAPDKAHKTCVTHLQSK	120		
Db	61	LVRPLAVFDAEGLRELGERSGFQTALKHECASSNDEILELARIAPDKAHKTCVTHLQSK	120		
QY	121	GRGRQGRKWSHRLGECIMFSGVWFDPRQYELGSLSPVAACRRALSRLGLDVQIKWPN	180		
Db	121	GRGRQGRKWSHRLGECIMFSGVWFDPRQYELGSLSPVAACRRALSRLGLDVQIKWPN	180		
QY	181	DLWVGRDKLGILIEVTGTGKTVAVVGIGINFVLPKEVENAASVQSLFQTSRRGNADA	240		

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OM protein - protein search, using sw model

Run on: June 24, 2003, 22:24:12 ; Search time 14.5605 Seconds
(without alignments)
1947.059 Million cell updates/sec

Title: US-09-813-453A-45
Perfect score: 1341
Sequence: 1 MIFVLDVGNNTNAVGLGVFEFG.....LKGLMYERNANLQHERGE 262

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 417779 seqs, 108206813 residues 417779
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/PCRUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1341	100.0	262	9	US-09-813-453A-45
2	1057.5	78.9	258	9	US-09-813-453A-49
3	1034	77.1	258	9	US-09-813-453A-2
4	960	71.6	254	9	US-09-813-453A-47
5	901	67.2	233	9	US-09-813-453A-17
6	802.5	59.8	256	9	US-09-813-453A-55
7	783	58.4	255	9	US-09-813-453A-7
8	665.5	49.6	250	9	US-09-813-453A-3
9	638	47.6	265	9	US-09-813-453A-4
10	566	42.2	260	9	US-09-813-453A-51
11	536	40.0	258	9	US-09-813-453A-6
12	527	39.3	219	9	US-09-813-453A-57
13	471.5	35.2	272	9	US-09-813-453A-5
14	467.5	34.9	272	9	US-09-712-363-276
15	405.5	30.2	262	9	US-09-813-453A-8
16	399.5	29.8	246	9	US-09-813-453A-9
17	379.5	28.3	212	9	US-09-813-453A-59
18	342.5	25.5	273	9	US-09-813-453A-10
19	316	23.6	257	9	US-09-813-453A-53

20	276.5	20.6	262	9	US-09-813-453A-11
21	207.5	15.5	244	9	US-09-813-453A-41
22	190.5	14.2	241	9	US-09-813-453A-63
23	169.5	12.6	592	9	US-09-813-453A-43
24	168	12.5	460	9	US-09-813-453A-39
25	168	12.5	592	9	US-09-813-453A-22
26	167.5	12.5	229	9	US-09-813-453A-12
27	156.5	11.7	257	9	US-09-813-453A-13
28	142	10.6	249	9	US-09-813-453A-61
29	138	10.3	267	9	US-09-813-453A-15
30	137	10.2	249	9	US-09-813-453A-70
31	136	10.1	248	9	US-09-813-453A-20
32	117	8.7	242	9	US-09-813-453A-65
33	113	8.4	209	9	US-09-813-453A-21
34	98.5	7.3	223	9	US-09-895-913A-74
35	98.5	7.3	223	9	US-09-813-453A-14
36	98.5	7.3	223	9	US-09-813-453A-67
37	97	7.2	509	10	US-09-815-242-5796
38	97	7.2	517	10	US-09-815-242-12837
39	90	6.7	294	10	US-09-815-242-13475
40	88.5	6.6	1019	1	US-08-834-705-18
41	86	6.4	357	9	US-10-012-896-826
42	86	6.4	357	9	US-09-895-793-826
43	86	6.4	357	9	US-09-895-814-826
44	86	6.4	357	10	US-09-759-143-826
45	86	6.4	357	10	US-09-780-669-826

ALIGNMENTS

RESULT 1

US-09-813-453A-45
; Sequence 45, Application US/09813453A
; Patent No. US20020168681A1

GENERAL INFORMATION:
; APPLICANT: Yocum, R. Rogers
; APPLICANT: Patterson, Thomas A.
; TITLE OF INVENTION: MICROORGANISMS AND ASSAYS FOR THE IDENTIFICATION OF
; TITLE OF INVENTION: ANTIBIOTICS
; FILE REFERENCE: OGZ-001
; CURRENT APPLICATION NUMBER: US/09/813,453A
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/227,860
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 09/667,569
; PRIOR FILING DATE: 2000-09-21
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Bacillus anthracis

US-09-813-453A-45

Query Match 100.0%; Score 1341; DB 9; Length 262;
Best Local Similarity 100.0%; Pred. No. 3.9e-121;
Matches 262; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MIFVLDVGNNTNAVGLGVFEFEGELRQHRWMDTRHKTDEYGMVLVKQLLEHGLSFEDVKGI	60
Db	1	MIFVLDVGNNTNAVGLGVFEFEGELRQHRWMDTRHKTDEYGMVLVKQLLEHGLSFEDVKGI	60
Qy	61	IVSSVPPIMFALERMCEKFKIKPLVVGPGIKTGLNLIKYPENREVGADRIYNVAGIHL	120
Db	61	IVSSVPPIMFALERMCEKFKIKPLVVGPGIKTGLNLIKYPENREVGADRIYNVAGIHL	120
Qy	121	YGSPLIIVDFGTATTTCYINEEKHYMGVITPGIMISAEALYRAAKLPRIETKPSVV	180
Db	121	YGSPLIIVDFGTATTTCYINEEKHYMGVITPGIMISAEALYRAAKLPRIETKPSVV	180
Qy	181	GKNTVSAMQSGILYGVGVGIVKRMKEAKQEPKVIATGGLAKLTSTESNVILVYQPF	240
Db	181	GKNTVSAMQSGILYGVGVGIVKRMKEAKQEPKVIATGGLAKLTSTESNVILVYQPF	240

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protein - protein search, using sw model

Run on: June 24, 2003, 22:24:12 ; Search time 14.1159 Seconds
(without alignments)
1947.059 Million cell updates/sec

Title: US-09-813-453A-47
Perfect score: 1293
Sequence: 1 MILVIDVGNNTVLGVYQDE.....DVIDSFLTKGLQLIYKKNV 254

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 417779 seqs, 108206813 residues 417779
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1293	100.0	254	9	US-09-813-453A-47
2	987	76.3	258	9	US-09-813-453A-2
3	975	75.4	258	9	US-09-813-453A-49
4	960	74.2	262	9	US-09-813-453A-45
5	862	66.7	233	9	US-09-813-453A-17
6	814.5	63.0	256	9	US-09-813-453A-55
7	771	59.6	255	9	US-09-813-453A-7
8	662	51.2	265	9	US-09-813-453A-4
9	648.5	50.2	250	9	US-09-813-453A-3
10	598	46.2	260	9	US-09-813-453A-51
11	528	40.8	258	9	US-09-813-453A-6
12	527	40.8	219	9	US-09-813-453A-57
13	487.5	37.7	272	9	US-09-813-453A-5
14	483.5	37.4	272	9	US-09-712-363-276
15	437.5	33.8	262	9	US-09-813-453A-8
16	389.5	30.1	246	9	US-09-813-453A-9
17	330.5	25.6	212	9	US-09-813-453A-59
18	322	24.9	257	9	US-09-813-453A-53
19	320.5	24.8	273	9	US-09-813-453A-10

20	275.5	21.3	262	9	US-09-813-453A-11	Sequence 11, Appl
21	197.5	15.3	244	9	US-09-813-453A-41	Sequence 41, Appl
22	179.5	13.9	241	9	US-09-813-453A-63	Sequence 63, Appl
23	138.5	10.7	229	9	US-09-813-453A-12	Sequence 12, Appl
24	137.5	10.6	257	9	US-09-813-453A-13	Sequence 13, Appl
25	137	10.6	460	9	US-09-813-453A-39	Sequence 39, Appl
26	137	10.6	592	9	US-09-813-453A-22	Sequence 22, Appl
27	136	10.5	592	9	US-09-813-453A-43	Sequence 43, Appl
28	131.5	10.2	267	9	US-09-813-453A-15	Sequence 15, Appl
29	121	9.4	248	9	US-09-813-453A-20	Sequence 20, Appl
30	117.5	9.1	249	9	US-09-813-453A-70	Sequence 70, Appl
31	114	8.8	249	9	US-09-813-453A-61	Sequence 61, Appl
32	110	8.5	209	9	US-09-813-453A-21	Sequence 21, Appl
33	107.5	8.3	242	9	US-09-813-453A-65	Sequence 65, Appl
34	91	7.0	223	9	US-09-895-913A-74	Sequence 74, Appl
35	91	7.0	223	9	US-09-813-453A-14	Sequence 14, Appl
36	91	7.0	223	9	US-09-813-453A-67	Sequence 67, Appl
37	84	6.5	225	9	US-09-738-626-4158	Sequence 4158, Ap
38	80.5	6.2	958	9	US-09-953-280-43	Sequence 43, Appl
39	80	6.2	343	9	US-10-060-432-28	Sequence 28, Appl
40	80	6.2	343	10	US-09-905-173-28	Sequence 28, Appl
41	79.5	6.1	518	9	US-09-738-626-4769	Sequence 4769, Ap
42	79	6.1	2492	10	US-09-991-258-3	Sequence 3, Appl
43	79	6.1	4834	9	US-10-097-534-27	Sequence 27, Appl
44	78.5	6.1	317	9	US-09-533-029-4	Sequence 4, Appl
45	78.5	6.1	317	9	US-10-286-264-114	Sequence 114, App

ALIGNMENTS

RESULT 1
US-09-813-453A-47
; Sequence 47, Application US/09813453A
; Patent No. US20020168681A1
; GENERAL INFORMATION:
; APPLICANT: Yocum, R. Rogers
; APPLICANT: Patterson, Thomas A.
; TITLE OF INVENTION: MICROORGANISMS AND ASSAYS FOR THE IDENTIFICATION OF
; TITLE OF INVENTION: ANTIBIOTICS
; FILE REFERENCE: OGZ-001
; CURRENT APPLICATION NUMBER: US/09/813,453A
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/227,860
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 09/667,569
; PRIOR FILING DATE: 2000-09-21
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Bacillus halodurans
US-09-813-453A-47

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Db	1	MILVIDVGNNTVLGVYQDETLVHHWRLATSRQKTEDEYAMTVRSFLDHAGLQFQDIDGI	60	Best Local Similarity	100.0%;	Pred. No. 2.8e-122;		
				Matches 254;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	61	VISSVVPMMFSLQMKCKYFHVTPMIIGPGIKTGLNKNPKEVGADRIYNAVAIAEL	120					
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Db	121	YGYPAIVVDFGTATTYCLINEKKQYAGGVIAPIAGIMISTEALYHRASKLPRIETAKPKQV	180					
QY	181	GTNTIDSMQSGIFYGVSVQDGVVKKMAQAESEPKVIATGGLAKLIGTSETIDVIDSF	240					

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OM protein - protein search, using sw model

Run on: June 24, 2003, 22:08:46 ; Search time 11.7629 Seconds
(without alignments)
2373.336 Million cell updates/sec

Title: US-09-813-453A-2
Perfect score: 1335
Sequence: 1 LLLVIDVGNNTVLGVYHDG.....PFLTLKGLIYERNRGSV 258

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 417779 seqs, 108206813 residues 417779

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1335	100.0	258	9	US-09-813-453A-2
2	1114	83.4	233	9	US-09-813-453A-17
3	1046	78.4	258	9	US-09-813-453A-49
4	1034	77.5	262	9	US-09-813-453A-45
5	987	73.9	254	9	US-09-813-453A-47
6	794.5	59.5	256	9	US-09-813-453A-55
7	756	56.6	255	9	US-09-813-453A-7
8	655	49.1	265	9	US-09-813-453A-4
9	646.5	48.4	250	9	US-09-813-453A-3
10	577	43.2	260	9	US-09-813-453A-51
11	537	40.2	258	9	US-09-813-453A-6
12	515	38.6	219	9	US-09-813-453A-57
13	494.5	37.0	272	9	US-09-813-453A-5
14	493.5	37.0	272	9	US-09-712-363-276
15	428	32.1	262	9	US-09-813-453A-8
16	405.5	30.4	246	9	US-09-813-453A-9
17	338.5	25.4	212	9	US-09-813-453A-59
18	327.5	24.5	273	9	US-09-813-453A-10
19	319	23.9	257	9	US-09-813-453A-53

20	271.5	20.3	262	9	US-09-813-453A-11	Sequence 11, Appl
21	207	15.5	244	9	US-09-813-453A-41	Sequence 41, Appl
22	203	15.2	241	9	US-09-813-453A-63	Sequence 63, Appl
23	163	12.2	249	9	US-09-813-453A-70	Sequence 70, Appl
24	163	12.2	257	9	US-09-813-453A-13	Sequence 13, Appl
25	154.5	11.6	229	9	US-09-813-453A-12	Sequence 12, Appl
26	154	11.5	249	9	US-09-813-453A-61	Sequence 61, Appl
27	151	11.3	460	9	US-09-813-453A-39	Sequence 39, Appl
28	150	11.2	592	9	US-09-813-453A-22	Sequence 22, Appl
29	150	11.2	592	9	US-09-813-453A-43	Sequence 43, Appl
30	134.5	10.1	242	9	US-09-813-453A-65	Sequence 65, Appl
31	133	10.0	248	9	US-09-813-453A-20	Sequence 20, Appl
32	129.5	9.7	267	9	US-09-813-453A-15	Sequence 15, Appl
33	109.5	8.2	223	9	US-09-895-913A-74	Sequence 74, Appl
34	109.5	8.2	223	9	US-09-813-453A-14	Sequence 14, Appl
35	109.5	8.2	223	9	US-09-813-453A-67	Sequence 67, Appl
36	109	8.2	209	9	US-09-813-453A-21	Sequence 21, Appl
37	80	6.0	449	10	US-09-815-242-5474	Sequence 5474, Ap
38	80	6.0	449	10	US-09-815-242-12348	Sequence 12348, A
39	80	6.0	449	10	US-09-815-242-12793	Sequence 12793, A
40	79	5.9	636	10	US-09-205-658-160	Sequence 160, App
41	78.5	5.9	337	9	US-10-075-846-12	Sequence 12, Appl
42	78.5	5.9	776	10	US-09-815-242-13811	Sequence 13811, A
43	78.5	5.9	1057	10	US-09-815-242-5798	Sequence 5798, Ap
44	78.5	5.9	1107	10	US-09-815-242-12815	Sequence 12815, A
45	78.5	5.9	1198	10	US-09-815-242-12446	Sequence 12446, A

ALIGNMENTS

RESULT 1

US-09-813-453A-2
; Sequence 2, Application US/09813453A
; Patent No. US20020168681A1
; GENERAL INFORMATION:
; APPLICANT: Yocum, R. Rogers
; APPLICANT: Patterson, Thomas A.
; TITLE OF INVENTION: MICROORGANISMS AND ASSAYS FOR THE IDENTIFICATION OF
; TITLE OF INVENTION: ANTIBIOTICS
; FILE REFERENCE: OGZ-001
; CURRENT APPLICATION NUMBER: US/09/813,453A
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/227,860
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 09/667,569
; PRIOR FILING DATE: 2000-09-21
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-09-813-453A-2

Query Match 100.0%; Score 1335; DB 9; Length 258;
Best Local Similarity 100.0%; Pred. No. 1.5e-129;
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	LLLVIDVGNNTVLGVYHDGKLEIYHWRISRKTEDEFGMILRSLEDSGLMFEQIDGI	50
Db	1	LLLVIDVGNNTVLGVYHDGKLEIYHWRISRKTEDEFGMILRSLEDSGLMFEQIDGI	60
QY	61	IISVVPPIMFALERMCTKYFHIEPQIVGPMKTLGNIKYDNPKVGALETVNVAAL	120
Db	61	IISVVPPIMFALERMCTKYFHIEPQIVGPMKTLGNIKYDNPKVGALETVNVAAL	120
QY	121	YGNPLIVVDFGTATTTCYIDENKQYMGGAIAPIGTISTEALYSAAKLPRIETRPDNI	180
Db	121	YGNPLIVVDFGTATTTCYIDENKQYMGGAIAPIGTISTEALYSAAKLPRIETRPDNI	190
QY	181	GKNTVSAMQSGILFGYGVGEGIVKRMKWOAKQDLKVIATGGLAPLIANESDCIDIVDPF	240

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protein - protein search, using sw model

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2373.336 Million cell updates/sec

Title: US-09-813-453A-7
Perfect score: 1279
Sequence: 1 MLLVIDVGNNTNIVLGIYDGE.....AVEEYLTLEGLRILYERNRE 255

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 417779 seqs, 108206813 residues
Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA:*
- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pap.*
 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pap.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pap.*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pap.*
 - 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pap.*
 - 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pap.*
 - 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pap.*
 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pap.*
 - 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pap.*
 - 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pap.*
 - 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pap.*
 - 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pap.*
 - 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pap.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1279	100.0	255	9	US-09-813-453A-7
2	834	65.2	258	9	US-09-813-453A-49
3	785.5	61.4	256	9	US-09-813-453A-55
4	783	61.2	262	9	US-09-813-453A-45
5	771	60.3	254	9	US-09-813-453A-47
6	756	59.1	258	9	US-09-813-453A-2
7	650	50.8	233	9	US-09-813-453A-17
8	631.5	49.4	250	9	US-09-813-453A-3
9	629	49.2	265	9	US-09-813-453A-4
10	561	43.9	260	9	US-09-813-453A-51
11	558	43.6	219	9	US-09-813-453A-57
12	554	43.3	258	9	US-09-813-453A-6
13	509.5	39.8	272	9	US-09-813-453A-5
14	505.5	39.5	272	9	US-09-712-363-276
15	414.5	32.4	262	9	US-09-813-453A-8
16	371.5	29.0	273	9	US-09-813-453A-10
17	361.5	28.3	246	9	US-09-813-453A-9
18	338.5	26.5	212	9	US-09-813-453A-59
19	301	23.5	257	9	US-09-813-453A-53

20	266.5	20.8	262	9	US-09-813-453A-11
21	208	16.3	244	9	US-09-813-453A-41
22	172.5	13.5	241	9	US-09-813-453A-63
23	163.5	12.8	249	9	US-09-813-453A-70
24	159	12.4	249	9	US-09-813-453A-61
25	148	11.6	267	9	US-09-813-453A-15
26	143	11.2	460	9	US-09-813-453A-39
27	141	11.0	248	9	US-09-813-453A-20
28	141	11.0	592	9	US-09-813-453A-22
29	139.5	10.9	229	9	US-09-813-453A-12
30	139.5	10.9	592	9	US-09-813-453A-43
31	128	10.0	242	9	US-09-813-453A-65
32	126	9.9	257	9	US-09-813-453A-13
33	100.5	7.9	223	9	US-09-895-913A-74
34	100.5	7.9	223	9	US-09-813-453A-14
35	100.5	7.9	223	9	US-09-813-453A-67
36	94	7.3	610	10	US-09-815-242-11183
37	89	7.0	317	12	US-10-043-238-1
38	89	7.0	317	12	US-10-043-238-3
39	86	6.7	387	10	US-09-925-300-1477
40	83.5	6.5	388	9	US-10-154-251-52
41	83	6.5	4551	9	US-09-793-708-1
42	82	6.4	485	9	US-09-738-626-4551
43	81.5	6.4	714	10	US-09-815-242-10266
44	80.5	6.3	398	10	US-09-815-242-10390
45	80.5	6.3	472	10	US-09-822-863-4

ALIGNMENTS

RESULT 1

US-09-813-453A-7
; Sequence 7, Application US/09813453A
; Patent No. US20020168681A1
; GENERAL INFORMATION:
; APPLICANT: Yocum, R. Rogers
; APPLICANT: Patterson, Thomas A.
; TITLE OF INVENTION: MICROORGANISMS AND ASSAYS FOR THE IDENTIFICATION OF
; TITLE OF INVENTION: ANTIBIOTICS
; FILE REFERENCE: OGZ-001
; CURRENT APPLICATION NUMBER: US/09/813,453A
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/227,860
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 09/667,569
; PRIOR FILING DATE: 2000-09-21
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Geobacter sulfurreducens
US-09-813-453A-7

QY	1	MLLVIDVGNNTNIVLGIYDGERLVRDWRVSTDKARTDEYGLINELFRLAGLGLDQIRAV	60
Db	1	MLLVIDVGNNTNIVLGIYDGERLVRDWRVSTDKARTDEYGLINELFRLAGLGLDQIRAV	60
QY	61	IISSVVPPLTGVLRLSLGYFGMRPLVVGPGIKTGMPIQYDNPREVGADRIYNAVAGYEK	120
Db	61	IISSVVPPLTGVLRLSLGYFGMRPLVVGPGIKTGMPIQYDNPREVGADRIYNAVAGYEK	120
QY	121	YRTSLIIVDFGTATTFDYVNRKGEYCGGAIAPGLVISTEALFQRASKLPKVDIIRPSALL	180
Db	121	YRTSLIIVDFGTATTFDYVNRKGEYCGGAIAPGLVISTEALFQRASKLPKVDIIRPSALL	180
QY	181	ARNTVNSMQAGIYYGVGLVDEIVTRMKAESKDAPRVATGGGLASLIAPESKTIYAVENY	240

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Protein search, using sw model

June 24, 2003, 22:08:46 ; Search time 11.3982 seconds
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2373.336 Million cell updates/sec

Title: US-09-813-453A-3
Perfect score: 1257
Sequence: 1 NKRAAFMLLLFLRSVLKVL.....GRRTRTSVLATGGLAKLIN 250

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 417779 seqs, 108206813 residues 417779
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA.*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1257	100.0	250	9 US-09-813-453A-3	Sequence 3, Appli
2	695	55.3	256	9 US-09-813-453A-55	Sequence 55, Appl
3	665.5	52.9	262	9 US-09-813-453A-45	Sequence 45, Appl
4	648.5	51.6	254	9 US-09-813-453A-47	Sequence 47, Appl
5	646.5	51.4	258	9 US-09-813-453A-2	Sequence 2, Appli
6	631.5	50.2	255	9 US-09-813-453A-7	Sequence 7, Appli
7	629.5	50.1	258	9 US-09-813-453A-49	Sequence 49, Appl
8	623	49.6	233	9 US-09-813-453A-17	Sequence 17, Appl
9	513	40.8	219	9 US-09-813-453A-57	Sequence 57, Appl
10	498.5	39.7	265	9 US-09-813-453A-4	Sequence 4, Appli
11	460.5	36.6	260	9 US-09-813-453A-51	Sequence 51, Appl
12	428.5	34.1	258	9 US-09-813-453A-6	Sequence 6, Appli
13	392	31.2	272	9 US-09-712-363-276	Sequence 276, App
14	389	30.9	272	9 US-09-813-453A-5	Sequence 5, Appli
15	337	26.8	262	9 US-09-813-453A-8	Sequence 8, Appli
16	333.5	26.5	246	9 US-09-813-453A-9	Sequence 9, Appli
17	327.5	26.1	212	9 US-09-813-453A-59	Sequence 59, Appl
18	282.5	22.5	273	9 US-09-813-453A-10	Sequence 10, Appl
19	262	20.8	262	9 US-09-813-453A-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-09-813-453A-3
; Sequence 3, Application US/09813453A
; Patent No. US20020168681A1
; GENERAL INFORMATION:
; APPLICANT: Yocum, R. Rogers
; APPLICANT: Patterson, Thomas A.
; TITLE OF INVENTION: MICROORGANISMS AND ASSAYS FOR THE IDENTIFICATION OF
; TITLE OF INVENTION: ANTIBIOTICS
; FILE REFERENCE: OGZ-001
; CURRENT APPLICATION NUMBER: US/09/813,453A
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/227,860
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 09/667,569
; PRIOR FILING DATE: 2000-09-21
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 3
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Clostridium acetobutylicum
US-09-813-453A-3

QY	1	NKRAAFMLLLFLRSVLKVLVDVGNINVLGIYNDTKLTAEWRLSTDVLRSADEYGIQV	60
DB	1	NKRAAFMLLLFLRSVLKVLVDVGNINVLGIYNDTKLTAEWRLSTDVLRSADEYGIQV	60
QY	61	MNLFQDQKLDPTLVEGVIISSVWPVNIMYSLEHMIRKYNPLVVGPGIKTGINKYDNP	120
DB	61	MNLFQDQKLDPTLVEGVIISSVWPVNIMYSLEHMIRKYNPLVVGPGIKTGINKYDNP	120
QY	121	KEVGADRVNVAHAHEIYKRSLLIIDFGTATTCFCAVRENGDYLGGAIKVSSEPLF	180
DB	121	KEVGADRVNVAHAHEIYKRSLLIIDFGTATTCFCAVRENGDYLGGAIKVSSEPLF	180
QY	181	KAALPRVELIKPAYAICKNTISSIQSGIVRYLRQVLYFEKLENLPUGKRTTSEVL	240
DB	181	KAALPRVELIKPAYAICKNTISSIQSGIVRYLRQVLYFEKLENLPUGKRTTSEVL	240

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OM protein - protein search, using sw model

Run on: June 24, 2003, 22:08:46 ; Search time 11.307 Seconds
(without alignments)
2373.336 Million cell updates/sec

Title: US-09-813-453A-20
Perfect score: 1248
Sequence: 1 MILEDCGNSLIKWRVIEGA.....GARIMPDVLFVGLALACPIE 248

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 417779 seqs, 108206813 residues 417779
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

1:	/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
2:	/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3:	/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4:	/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5:	/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1248	100.0	248	9	US-09-813-453A-20
2	794.5	63.7	249	9	US-09-813-453A-61
3	789.5	63.3	249	9	US-09-813-453A-70
4	234.5	18.8	592	9	US-09-813-453A-43
5	232.5	18.6	460	9	US-09-813-453A-39
6	231.5	18.5	592	9	US-09-813-453A-22
7	195.5	15.7	244	9	US-09-813-453A-41
8	193	15.5	242	9	US-09-813-453A-65
9	178.5	14.3	267	9	US-09-813-453A-15
10	160	12.8	260	9	US-09-813-453A-51
11	159.5	12.8	223	9	US-09-895-913A-74
12	159.5	12.8	223	9	US-09-813-453A-14
13	159.5	12.8	223	9	US-09-813-453A-67
14	159.5	12.8	250	9	US-09-813-453A-3
15	157	12.6	257	9	US-09-813-453A-53
16	149	11.9	272	9	US-09-813-453A-5
17	147	11.8	272	9	US-09-712-363-276
18	145	11.6	246	9	US-09-813-453A-9
19	144.5	11.6	241	9	US-09-813-453A-63

20	141	11.3	255	9	US-09-813-453A-7	Sequence 7, Appli
21	138.5	11.1	265	9	US-09-813-453A-4	Sequence 4, Appli
22	136	10.9	219	9	US-09-813-453A-57	Sequence 57, Appli
23	136	10.9	258	9	US-09-813-453A-6	Sequence 6, Appli
24	136	10.9	262	9	US-09-813-453A-45	Sequence 45, Appli
25	136	10.9	273	9	US-09-813-453A-10	Sequence 10, Appli
26	133	10.7	258	9	US-09-813-453A-2	Sequence 2, Appli
27	123.5	9.9	258	9	US-09-813-453A-49	Sequence 49, Appli
28	121	9.7	254	9	US-09-813-453A-47	Sequence 47, Appli
29	120.5	9.7	209	9	US-09-813-453A-21	Sequence 21, Appli
30	119.5	9.6	256	9	US-09-813-453A-55	Sequence 55, Appli
31	111	8.9	233	9	US-09-813-453A-17	Sequence 17, Appli
32	107	8.6	212	9	US-09-813-453A-59	Sequence 59, Appli
33	107	8.6	257	9	US-09-813-453A-13	Sequence 13, Appli
34	98.5	7.9	229	9	US-09-813-453A-12	Sequence 12, Appli
35	89	7.1	4150	9	US-09-808-880-2	Sequence 2, Appli
36	88.5	7.1	277	9	US-09-738-626-4512	Sequence 4512, Ap
37	86	6.9	277	9	US-09-738-626-4732	Sequence 4732, Ap
38	85	6.8	298	9	US-09-712-363-253	Sequence 253, App
39	84	6.7	956	10	US-09-815-242-11925	Sequence 11925, A
40	84	6.7	1827	9	US-09-712-363-261	Sequence 261, App
41	83.5	6.7	262	9	US-09-813-453A-11	Sequence 11, Appli
42	83	6.7	392	10	US-09-945-825-8	Sequence 8, Appli
43	83	6.7	467	10	US-09-841-880-4	Sequence 4, Appli
44	82.5	6.6	251	10	US-09-815-242-12053	Sequence 12053, A
45	82.5	6.6	258	9	US-09-712-363-220	Sequence 220, App

ALIGNMENTS

RESULT 1

US-09-813-453A-20
; Sequence 20, Application US/09813453A
; Patent No. US20020168681A1
; GENERAL INFORMATION:
; APPLICANT: Yocum, R. Rogers
; APPLICANT: Patterson, Thomas A.
; TITLE OF INVENTION: MICROORGANISMS AND ASSAYS FOR THE IDENTIFICATION OF
; TITLE OF INVENTION: ANTIBIOTICS
; FILE REFERENCE: OG2-001
; CURRENT APPLICATION NUMBER: US/09/813,453A
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/227,860
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 09/667,569
; PRIOR FILING DATE: 2000-09-21
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-813-453A-20

Query Match 100.0%; Score 1248; DB 9; Length 248
Best Local Similarity 100.0%; Pred. No. 1.3e-117;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	181	AEAVRGCLLMRLRGFVREQYAMACELGPDCEIFLTGGDAELVRDELACARIMPDVFG 240	

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protein search, using sw model

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Title: US-09-813-453A-61
Perfect score: 1269
Sequence: 1 MILEDCGNSFIKRWIVHVA.....QARVVPDLVFLVGLAMACPLD 249

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1269	100.0	249	9	US-09-813-453A-61
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3	794.5	62.6	248	9	US-09-813-453A-20
4	245	19.3	592	9	US-09-813-453A-43
5	243	19.1	592	9	US-09-813-453A-22
6	232	18.3	460	9	US-09-813-453A-39
7	210	16.5	265	9	US-09-813-453A-4
8	181	14.3	244	9	US-09-813-453A-41
9	168.5	13.3	242	9	US-09-813-453A-65
10	163	12.8	267	9	US-09-813-453A-15
11	160.5	12.6	272	9	US-09-813-453A-5
12	159	12.5	255	9	US-09-813-453A-7
13	157.5	12.4	272	9	US-09-712-363-276
14	156	12.3	250	9	US-09-813-453A-3
15	154	12.1	258	9	US-09-813-453A-2
16	153.5	12.1	260	9	US-09-813-453A-51
17	144.5	11.4	223	9	US-09-895-913A-74
18	144.5	11.4	223	9	US-09-813-453A-14
19	144.5	11.4	223	9	US-09-813-453A-67

20	142	11.2	262	9	US-09-813-453A-45	Sequence 45, Appl
21	139	11.0	258	9	US-09-813-453A-49	Sequence 49, Appl
22	134	10.6	219	9	US-09-813-453A-57	Sequence 57, Appl
23	131	10.3	256	9	US-09-813-453A-55	Sequence 55, Appl
24	130.5	10.3	257	9	US-09-813-453A-53	Sequence 53, Appl
25	129.5	10.2	233	9	US-09-813-453A-17	Sequence 17, Appl
26	124	9.8	258	9	US-09-813-453A-6	Sequence 6, Appl
27	118	9.3	257	9	US-09-813-453A-13	Sequence 13, Appl
28	118	9.3	273	9	US-09-813-453A-10	Sequence 10, Appl
29	117.5	9.3	246	9	US-09-813-453A-9	Sequence 9, Appl
30	117	9.2	277	9	US-09-738-626-4732	Sequence 4732, Ap
31	114.5	9.0	209	9	US-09-813-453A-21	Sequence 21, Appl
32	114.5	9.0	212	9	US-09-813-453A-59	Sequence 59, Appl
33	114	9.0	254	9	US-09-813-453A-47	Sequence 47, Appl
34	104.5	8.2	241	9	US-09-813-453A-63	Sequence 63, Appl
35	95	7.5	262	9	US-09-813-453A-8	Sequence 8, Appl
36	92.5	7.3	229	9	US-09-813-453A-12	Sequence 12, Appl
37	90	7.1	1832	9	US-10-014-717-4	Sequence 4, Appl
38	89	7.0	218	9	US-09-738-626-6401	Sequence 6401, Ap
39	87.5	6.9	540	9	US-09-712-363-169	Sequence 169, App
40	87.5	6.9	540	9	US-10-267-311-4	Sequence 4, Appl
41	87.5	6.9	540	9	US-10-046-649-4	Sequence 4, Appl
42	87.5	6.9	540	10	US-09-847-637B-6	Sequence 6, Appl
43	87.5	6.9	639	9	US-10-267-311-17	Sequence 17, Appl
44	87.5	6.9	648	9	US-10-267-311-29	Sequence 29, Appl
45	87.5	6.9	690	9	US-10-068-059-10	Sequence 10, Appl

ALIGNMENTS

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US-09-813-453A-61

; Sequence 61, Application US/09813453A

; Patent No. US20020168681A1

; GENERAL INFORMATION:

; APPLICANT: Yocum, R. Rogers

; APPLICANT: Patterson, Thomas A.

; TITLE OF INVENTION: MICROORGANISMS AND ASSAYS FOR THE IDENTIFICATION OF

; TITLE OF INVENTION: ANTIBIOTICS

; FILE REFERENCE: OGZ-001

; CURRENT APPLICATION NUMBER: US/09/813,453A

; CURRENT FILING DATE: 2001-03-20

; PRIOR APPLICATION NUMBER: US 60/227,860

; PRIOR FILING DATE: 2000-08-24

; PRIOR APPLICATION NUMBER: 09/667,569

; PRIOR FILING DATE: 2000-09-21

; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 61

; LENGTH: 249

; TYPE: PRT

; ORGANISM: Pseudomonas putida

US-09-813-453A-61

Query Match 100.0%; Score 1269; DB 9; Length 249;
Best Local Similarity 100.0%; Pred. No. 1.1e-116;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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protein search, using sw model

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Perfect score: 1367
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5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1367	100.0	272	9 US-09-813-453A-5	Sequence 5, Appli
2	1363	99.7	272	9 US-09-712-363-276	Sequence 276, App
3	698.5	51.1	265	9 US-09-813-453A-4	Sequence 4, Appli
4	513	37.5	256	9 US-09-813-453A-55	Sequence 55, Appl
5	509.5	37.3	255	9 US-09-813-453A-7	Sequence 7, Appli
6	494.5	36.2	258	9 US-09-813-453A-2	Sequence 2, Appli
7	487.5	35.7	254	9 US-09-813-453A-47	Sequence 47, Appl
8	479.5	35.1	258	9 US-09-813-453A-49	Sequence 49, Appl
9	471.5	34.5	262	9 US-09-813-453A-45	Sequence 45, Appl
10	431.5	31.6	258	9 US-09-813-453A-6	Sequence 6, Appli
11	412	30.1	233	9 US-09-813-453A-17	Sequence 17, Appl
12	404	29.6	262	9 US-09-813-453A-8	Sequence 8, Appli
13	389	28.5	250	9 US-09-813-453A-3	Sequence 3, Appli
14	382.5	28.0	260	9 US-09-813-453A-51	Sequence 51, Appl
15	371	27.1	219	9 US-09-813-453A-57	Sequence 57, Appl
16	286	20.9	246	9 US-09-813-453A-9	Sequence 9, Appli
17	274.5	20.1	257	9 US-09-813-453A-53	Sequence 53, Appl
18	254	18.6	273	9 US-09-813-453A-10	Sequence 10, Appl
19	209.5	15.3	212	9 US-09-813-453A-59	Sequence 59, Appl

20	160.5	11.7	249	9 US-09-813-453A-61	Sequence 61, Appl
21	159	11.6	241	9 US-09-813-453A-63	Sequence 63, Appl
22	153	11.2	244	9 US-09-813-453A-41	Sequence 41, Appl
23	152	11.1	592	9 US-09-813-453A-22	Sequence 22, Appl
24	150.5	11.0	249	9 US-09-813-453A-70	Sequence 70, Appl
25	149	10.9	248	9 US-09-813-453A-20	Sequence 20, Appl
26	147.5	10.8	592	9 US-09-813-453A-43	Sequence 43, Appl
27	146.5	10.7	460	9 US-09-813-453A-39	Sequence 39, Appl
28	138	10.1	262	9 US-09-813-453A-11	Sequence 11, Appl
29	115	8.4	338	9 US-09-975-719-47	Sequence 47, Appl
30	114	8.3	229	9 US-09-813-453A-12	Sequence 12, Appl
31	112	8.2	242	9 US-09-813-453A-65	Sequence 65, Appl
32	106	7.8	257	9 US-09-813-453A-13	Sequence 13, Appl
33	100.5	7.4	264	9 US-09-712-363-183	Sequence 183, App
34	94	6.9	317	12 US-10-043-238-1	Sequence 1, Appli
35	94	6.9	317	12 US-10-043-238-3	Sequence 3, Appli
36	92.5	6.8	267	9 US-09-813-453A-15	Sequence 15, Appl
37	92	6.7	1510	9 US-09-738-626-3707	Sequence 3707, Ap
38	91.5	6.7	209	9 US-09-813-453A-21	Sequence 21, Appl
39	89.5	6.5	223	9 US-09-895-913A-74	Sequence 74, Appl
40	89.5	6.5	223	9 US-09-813-453A-14	Sequence 14, Appl
41	89.5	6.5	223	9 US-09-813-453A-67	Sequence 67, Appl
42	89	6.5	326	10 US-09-905-176-9	Sequence 9, Appli
43	89	6.5	337	10 US-09-815-242-12096	Sequence 12096, A
44	88	6.4	328	9 US-10-164-433-4	Sequence 4, Appli
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ALIGNMENTS

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; Sequence 5, Application US/09813453A
; Patent No. US20020168681A1
; GENERAL INFORMATION:
; APPLICANT: Yocum, R. Rogers
; APPLICANT: Patterson, Thomas A.
; TITLE OF INVENTION: MICROORGANISMS AND ASSAYS FOR THE IDENTIFICATION OF
; TITLE OF INVENTION: ANTIBIOTICS
; FILE REFERENCE: OG2-001
; CURRENT APPLICATION NUMBER: US/09/813,453A
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/227,860
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 09/667,569
; PRIOR FILING DATE: 2000-09-21
; NUMBER OF SEQ ID NOS: 77
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; SEQ ID NO 5
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; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-813-453A-5

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